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Pacents C. Application US/0794245

Pacent No. 563941

GREEAL MINCHARTON:

APPLICANT: SERALE, SEPPEN N.J.

ANDERSONGENCES: 522

COMERN: D.C.

STATE: D.C
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CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 179
LENGTH: 1776
TYPE: PRT
ORGANISM: Chlamydia

825 TPTLIGGGAI 834

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Gaps

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64.2%; Score 34; DB 4; Length 1776; 60.0%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels

Local Similarity 60.0

Matches

US-09-556-877-179

Query Match

|| : ||||: 825 TPTLIGGGAI 834

US-09-620-412C-179

1 TPRVTGGGAM 10

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Sequence 179, Application US/09620412C

Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND FILE REPRENCE: 2010.121.469C7
GURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT PILLICATION NUMBER: US/09/620,412C
CURRENT PILLICATION NUMBER: US/09/620,412C
NUMBER OF SEQ ID NGS: 363
SOFTWARE: FASTERO for Mindows Version 3.0/4.0

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                Sequence 179, Application US/09598419
Fatent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: 10121.46906
GURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                               64.2%; Score 34; DB 4; Length 1776; 60.0%; Pred. No. 1.4e+03; tive 2; Mismatches 2; Indels
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Chlamydia
US-09-598-419-179
                                                                                                                                                                                                                                                                                        SEQ ID NO 179
LENGTH: 1776
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RESULT 49 US-07-942-245-2

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Sequence 39, Application US/09240274

Sequence 39, Application US/09240274

Sequence 39, Application US/09240274

Sequence 39, Application US/09240274

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: SCHING METHOD FOR PRODUCTION THEREOF

FILE'REFERENCE: 09596-42U2

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/080,550

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER APPLICATION NUMBER: 1998-01-011

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 107
                                                                    GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RAID-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

CURRENT PELLING DATE: 1999-01-29

EARLIER FILING DATE: 1999-01-29

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.3%; Score 33; DB 3; Length 107
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 108
US-09-240-274-39
                         ; Sequence 38, Application US/09240274; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 TPRTFGGG 100
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US-09-240-274-38
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LENGTH: 107
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Gaps

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64.2%; Score 34; DB 4; Length 1776; 60.0%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels

Best Local Similarity 60.0 Matches 6; Conservative

ORGANISM: Chlamydia

TYPE: PRT

SEQ ID NO 179 LENGTH: 1776

US-09-620-412C-179

Query Match

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1 TPRVTGGGAM 10

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154 PTVAGGGAL 162

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TUBERCULOSIS
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APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 34; DB 4; Length 943; ilarity 66.7%; Pred. No. 7.6e+02; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILLING DATE: 05-MAY-1998
CLASSIFICATION:
            NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 4; I
Pred. No. 7.6e+02;
1; Mismatches 2;
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FILE REFERENCE: 52888
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 2000-01-03
PRIOR PELING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR PLING DATE: 1996-06-14
PRIOR PILING DATE: 1996-06-15
NUMBER OF SEQ ID NOS: 169
SEQ ID NO 131
LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-477-135A-131
; Sequence 131, Application US/09477135A
; Patent No. 6572865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECONO.
TELEPHONE: (206) 622-49vv
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%
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                                                                                                                 Washington
FITTE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
APPLICANT: Shing, Steve
APPLICANT: Filing, Steve
APPLICANT: FILING, Steve
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL, INFECTION
                                                                                                                                               APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Netc, Antonio
APPLICANT: Campos Netc, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronalel G.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: AND DIAGNOSIS OF TUBERCULOSIS
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.2%; Score 34; DB 4; Length 943; 66.7%; Pred. No. 7.6e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: "LOSA COUNTRY: USA ZELP: 94104-7092

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IRM PC COMPATIBLE COMPUTER: PACENCY SOFTWAND: SOFTWAND: PACENCY ACTOR SOFTWAND: APPLICATION DATA: APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 179, Application US/09556877; Patent No. 6432916; GENERAL INFORMATION:
                                            Sequence 204, Application US/09072967; Patent No. 6592877; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 210121.469C5
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amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
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RESULT 43
US-09-072-967-204
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Patent No. 6448234
GENERAL INFORMATION:
TELEMETAL INFORMATION:
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TILLE REFERENCE: 210121.46597
TILLE REFERENCE: 210121.46597
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 195
INSTITE OF INVENTION NUMBER: US/09/620,412C
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
MANNER PART NUMBER OF SEQ ID NOS: 363
MANNER NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                   APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARES: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 195, Application US/09598419
Faterin Wo. 6565866
GENERAL INFORMATION:
APPLICANT: SKelky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46966
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
IENGTH: 821
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                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 34; DB 4; Length 821; 60.0%; Pred. No. 6.7e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 TPTLIĞĞĞAI 821
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812 TPTLIGGGAI 821
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                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Chlamydia
US-09-620-412C-195
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; ORGANISM: Chlamydia
US-09-598-419-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-620-412C-195
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APPLICANT:
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
AUTILE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Query Match

64.2%; Score 34; DB 4; Length 821;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             ; Sequence 204, Application US/09056556; Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.74,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                             812 rPTLIGGGAI 821
                                                                                     1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-09-056-556-204
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US-09-072-596-199
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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265 PRTVGGGA 272
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                                                                                                                                                                US-09-598-419-357
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APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
MITLE OF INVENTION:
ABTOLIELE ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
RRIOR FILING DATE: 1996-07-27
NUMBER: OS 60/094,190
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

FILE REPRENEUR: 210121.469C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: PARESEQ FOR Windows Version 3.0/4.0
                                                                                                                                                                                                                                  Query Match

64.2%; Score 34; DB 1; Length 375;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.2%; Score 34; DB 4; Length 510; 75.0%; Pred. No. 4.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.2%; Score 34; DB 4; Length 683; 60.0%; Pred. No. 5.6e+02; Live 2; Mismatches 2; Indels
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
             TELEPHONE: (716) 856-4000
TELEPAX: (716) 849-0349
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-736-361A-5
                                                                                                                                                                                                                                                                                                                                                                341 PRVTSGGS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 PRTAGGGA 174
                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        2 PRVTGGGA 9
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US-09-252-991A-33084
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LENGTH: 683
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 52115
LENGTH: 717
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                                                                                                                                                                                                                                                APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENITON: COMPOUNDS AND METHODS FOR TREATMENT AND FILE BEPERENCE: 210121.46906
CURRENT PEPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 683;
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Guery Match

Guery Match

64.2%; Score 34; DB 4; Length 717;

Best Local Similarity 75.0%; Pred. No. 5.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels
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; Patent No. 6551795
                                                                                                                                                                                 Sequence 357, Application US/09598419 Patent No. 6565856
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Patent No. 6432916
GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0
Matches 6; Conservative
                                              258 rPTLIGGGAI 267
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1 TPRVTGGGAM 10
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                          Score 34; DB 4; Length 247; Pred. No. 2.2e+02; 1; Mismatches 1; Indels
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1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Lao, Guifang
TITLE OF INVENTION: Nucleotide Sequences encoding a
TITLE OF INVENTION: Thermostable Alkaline Protease
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM COMPATIBLE
OPREATING SYSTEM: MS-DOS, Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/736,361A
FILING DATE: 23 October 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Scor. No. 50. 85.7%; Pred. No. 50.
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                                                                                                                                                                                                                                                                                                                           Sequence 24996, Application US/09252991A Patent No. 6551795
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-414-828A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/08736361A; Patent No. 5705379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,300
                                                                                       Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7-
6, Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                     35 PKSTGGGA 42
                                                                                                                                                                             2 PRVTGGGA 9
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                                                                                                                                                                                                                                                                                                    US-09-252-991A-24996
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APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
               APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24671
LENGTH: 1150
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Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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Sequence 14, Application US/09414828A

Patent No. 6300084

GENERAL INFORMATION:
APPLICANT: Drubin, David G.
TITLE OF INVENTION: Anti-Mitchic Agents and Processes
FILE REPERENCE: Mitchic Spindle Proteins
CURRENT APLICATION NUMBER: US/09/414,828A

CURRENT FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 60/103,684

PRIOR FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 71, Application US/09325932A
Patent No. 6451604
                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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75.0%;
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Best Local Similarity 75.۰۰
اتم و ( Conservative  قرار کارپوری
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
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US-09-325-932A-71
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-24671
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LENGTH: 247
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.138
FILE REFERENCE: 107196.138
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
STO IN 02 29670
STO IN 02 29670
LENGTH: 269
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APPLICANT: Collmer, Alan
APPLICANT: Charkowski, Amy
APPLICANT: Alfano, James R.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM
TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 4; Length 369;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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Pred. No. 2.5e+02;
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ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYERN Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Misk
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L.
REGISTATION NUMBER: 30,720
REFERENCE/DOCKET NUMBER: 19603/1741
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,107
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-120-817-2
; Sequence 2, Application US/09120817
; Patent No. 6172184
                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INPORMATION FOR SEQ ID.NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%;
66.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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: U.S.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-29670
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27068
LENGTH: 638
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                                                                                                                                                                                    Sequence 14, Application US/09431614
Facent No. 6624139
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
TITLE OF INVENTION RESISTANCE
FILE REPERRENCE: 21829/41 (BBC-003)
CURRENT FILING DATE: 1999-11-02
RARLIER PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOSE: 18
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    Indels
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    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 27
US-09-252-991A-27068
; Sequence 27068, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
US-09-252-991A-24671
; Sequence 24671, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
  6; Conservative
                                                                                    169 TPTATGGGS 177
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                                            1 TPRVTGGGA 9
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US-09-431-614-14
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US-09-731-166-12
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LENGTH: 799
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Fatent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ALGORITHM AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 33082
LENGTH: 460
            APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27680
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                              69.8%; Score 37; DB 4; Length 289;
87.5%; Pred. No. 81;
Live 0; Mismatches 1; Indels
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; Patent No. 6107060
; GENERAL INFORMATION:
   APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hamping
: TITLE OF INVENTION: Starch Encapsulation
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 5370 Manhattan Circle
; CITY: Boulder
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.5
Matches 7; Conservative
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Matches 6; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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## Setent No. 6639126

## APPLICANT: Sewalt, Vincent J. H.

## APPLICANT: Singletary, George W.

## TITLE OF INVENTION: FOOTOUCTION OF Modified Polysaccarides

## TITLE OF INVENTION: POCOUCTION OF MODIFIES

## CURRENT APPLICATION NUMBER: US/09/731,166

## CURRENT APPLICATION NUMBER: US/09/731,166

## PRIOR FILING DATE: 1999-12-06

## PRIOR FILING DATE: 1999-12-06

## NUMBER OF SEQ ID NOS: 16

## NUMBER OF SEQ ID NOS: 16
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85.7%; Pred. No. 3.1e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 36; DB 3; Length 799; 85.7%; Pred. No. 3.1e+02; cive 1; Mismatches 0; Indels
                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A FILLING DATE: 30-SEP-1997 CLASSIFICATION: 800
                                                                                                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-628-1996
ATTOCNEY AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 29670, Application US/09252991A ; Patent No. 6551795
                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
IYPE: amino acid
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-941-445A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 PRLTGGG 23
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US-09-252-991A-29670
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us-10-697-055-7.rai

Page 10

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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC; OTHER INFORMATION: SEQUENCE
US-09-230-421-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC OTHER INFORMATION: SEQUENCE
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                                                                                                                                                                                          73.6%; Score 39; DB 2; Length 447; 77.9%; Pred. No. 58; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  US-09-230-421-13

US-09-230-421-13

Sequence 13, Application US/09230421

Patent No. 6200577

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: THEREPOR

TITLE OF INVENTION: THEREPOR

TITLE OF INVENTION: THEREPOR

TILE REFERENCE: P18189C

CURRENT APPLICATION UNDERR: US/09/230,421

CURRENT FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 14

SOFUTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.7%; Score 38; DB 3; Length 19; 100.0%; Pred. No. 4.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nedical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P18189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
            TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                         : 447 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                            Local Similarity 77.8 1es 7; Conservative
                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                            332 PRVPGGGAL 340
                                                                                                                                                                                                                                                                     2 PRVTGGGAM 10
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13 TPRVTGG 19
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SEQ ID NO 3
LENGTH: 144
                                                                                                                                                     US-08-468-857-2
                                                                       LENGTH:
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                                                                                                                                                                                          Query Match
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71.7%; Score 38; DB 3; Length 144;

Query Match

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: 107196_136
CURRENT PAPPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 2154
LENGTH: 455
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APPLICANT: LYND DOUGETEE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BATEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
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                                     Gaps
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71.7%; Score 38; DB 4; Length 455;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.8%; Score 37; DB 4; Length 125; 66.7%; Pred. No. 37; tive 1; Mismatches 2; Indels
                                     Indels
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Pred. No. 29;
                                                                                                                                                                                                                                                 Sequence 22154, Application US/09252991A
Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 66.7
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                                                                                                                             138 TPRVTGG 144
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1 PRIIGGGGM 9
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LENGTH: 125
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| Patent No. 5792644
| GENERAL INFORMATION:
| APPLICANT: van den BOCGARRT, Paul APPLICANT: VERWEULEN, Arnoldus Nicolaas
| TILLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Akzo No. 5792644el Patent Department
| STREET: 1300 Piccard Drive
| STREET: Maryland
| CONTRIBET: Maryland
                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,852
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
ADDRESSEE: Biotechnology Research Institute
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91.201.523.7
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/904,075
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: William M. Blackstone
REGISTRATION NUMBER: 29,772
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                   STREET: 1330-A Piccard Drive CITY: Rockville
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 447 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-310-357-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 PRVPGGGAL 340
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                                                                    STATE: Maryland COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                20850
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73.6%; Score 39; DB 1; Length 447;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,857
FILING DATE: 06-JUN 1995
CLASSIFICATION NUMBER: US/08/468,857
FILING DATE: 12-8EP-1994
PRIOR APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-8EP-1994
PRIOR APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
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1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08468857
Fatent No. 5925347
GENERAL INFORMATION:
APPLICANT: Van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERNEULEN, Arnoldus Nicolaas
ITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-Unn-1991
ATTONNEY, AGENT INFORMATION:
NAME: MALY E. GGRENLEY
REGISTRATION NUMBER: 34,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: protein US-08-468-852-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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STATE: Maryland
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 130
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US-08-468-857-2
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RESULT 12
US-08-468-855-2
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                                                            Query Match

90.6%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: LODGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Akzo No. 5670362el Patent Department
STREET: 1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: van den BOCGAART, Paul
APPLICANT: VK, Jacobus Johannus
APPLICANT: VERKHÜLEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NÜMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5670362el Patent Departmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,853
FILING DATE: 06-UTN-1995
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 12-SEP-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-A02-1993
FILING DATE: 18-UN-1992
FILING DATE: 18-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING ADATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
; OTHER INFORMATION: Xaa = L, F or M
US-09-692-170C-B
                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08468853
Patent No. 5670362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mary B. Gormley
REGISTRATION NUMBER: 34,409
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville STATE: Maryland
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US-08-468-853-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,855
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08310357

Patent No. 5789233
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: van den BOOGAART, Paul
APPLICANT: VOR, Jacobus Johannus
APPLICANT: VERWEULEN, Arnoldus Nicolaas
ITITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
                                                                                                                                                                                                                         ADDRESSEE: Akzo No. 5780289el Patent Department STREET: 1300 Piccard Drive CITY: Rockville STATE: Maryland COUNTRY: U.S.A.
Sequence 2, Application US/08468855
Patent No. 5780289
GENERAL INFORMATION:
APPLICANT: Van den BOOGAART, Paul
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-UUN-1991
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-UUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mary E. Gormley
REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 447 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 PRVPGGGAL 340
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US-08-310-357-2
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GENERAL INFORMATION:

APPLICANT: DIAMOND, DON JEFFREY

APPLICANT: YORK, JOANNE

TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: BART G. NEWLAND

STREET: 555 13TH STREET, NW SUITE 701E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%; Score 48; DB 3; Length 10;
100.0%; Pred. No. 0.054;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,257A
FILING DATE: 11-MAY-1998
CLASSIFICATION 1424
FILING DATE: 11-MAY-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1997
FILING DATE: 14-OCT-1997
PRIOR APPLICATION NUMBER: US 08/950,064
FILING DATE: 14-OCT-1997
RICH APPLICATION NUMBER: US 08/950,064
FILING DATE: 12-NOV-1996
ATTONINY/AGENT INFORMATION:
NAME: NEMLAND, BART G
REGISTRATION NUMBER: 31,282
REGISTRATION NUMBER: 31,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 10
; OTHER INFORMATION: /note= "Xaa = Leu, Phe, or Met"
US-09-075-257A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                   Sequence 8, Application US/09075257A
Patent No. 6074645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.6
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                             163 TPRVTGGGAM 172
1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain
LOCATION: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20004
                                                                                                                                                                                                                          JS-09-075-257A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Sequence 8, Application US/09692170C

Patent No. 6562345

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REPERENCE: 1954-346

CURRENT APPLICATION NUMBER: US/09/692,170C

CURRENT APPLICATION NUMBER: US/09/692,170C

CURRENT FILING DATE: 2000-10-20

PRIOR PILING DATE: 1998-05-11

PRIOR PELING DATE: 1998-05-11

PRIOR PELICATION NUMBER: US 09/025,257

PRIOR PELING DATE: 1998-05-11

PRIOR PELING DATE: 1998-05-11

PRIOR PELING DATE: 1998-05-10

PRIOR PELING DATE: 1998-05-10

PRIOR PELING DATE: 1998-05-10

PRIOR PELING DATE: 1998-02-10

PRIOR PELING DATE: 1998-02-10

PRIOR PELING DATE: 1997-10-14

PRIOR PELING DATE: 1997-10-14

PRIOR PELING DATE: 1996-11-12

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 8

LENGTH. 10

LENGTH. 10
Sequence 8, Application US/09534639
Patent No. 6251399
GENERAL INPORMATION:
APPLICANT: York, Joanne
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN
TITLE OF INVENTION: CYTOMEGALOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Human OTHER INFORMATION: Cytomegalovirus Epitope Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
90.6%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                        FILE REFERENCE: 1954-343
CURRENT APPLICATION NUMBER: US/09/534,639
CURRENT FILING DATE: 2000-03-27
EARLIER APPLICATION NUMBER: 09/075,257
EARLIER APPLICATION NUMBER: 09/01,298
EARLIER FILING DATE: 1998-05-11
EARLIER FILING DATE: 1998-02-10
EARLIER FILING DATE: 1998-02-10
EARLIER FILING DATE: 1997-10-14
EARLIER FILING DATE: 1997-10-14
EARLIER FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 20
SEQTTAARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa = Leu, Phe or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
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NAME/KEY: MISC_FEATURE
LOCATION: (10)..(10)
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US-09-692-170C-8
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Gaps

US-09-534-639-8

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                   COMPUTER READBALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATE: US/09/171,699
FILING DATE: 19-Jan-1999
CLASSIFICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOALFOLF, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WSTGGAPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9206
; SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
                     ADDRESSEE: Howson and Howson STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 53; DB 4; Length 579; Best Local Similarity 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Wistar Institute of, Anatomy & Biology
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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APPLICATION NUMBER: US/09/171,699
FILING DATE: 19-Jan-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/09171699; Patent No. 6448389; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gonczol, Eva
Berencsi, Klara
Kari, Csaba
                                                                                         STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                      Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-171-699-6
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100.0%; Score 53; DB 1; Length 631;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 53; DB 4; Length 579; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bruggeman, Catharina A.
APPLICANT: Wink, Cornelis
APPLICANT: Ramen, Albert
APPLICANT: Stals, Frans
TITLE OF INVENTION: A HUMAN CYTOMEGALOVIRUS COMBINED
TITLE OF INVENTION: A NUMBEN AND ITS USE
                  FILLING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOGNOFÉ, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,080
REFERENCE/DOCKET NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 322-5070
SRQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
APPLICATION NUMBER: US 60/015,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CTY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCIII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,541B
FILING DATE: February 22, 1996
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08605541B
Patent No. 5800981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 TPRVTGGGAM 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPRVTGGGAM 10
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Kari, Csaba
TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and
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TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: GZ 209500
CURRENT APPLICATION NUMBER: US/09/812,079A
CURRENT FILING DATE: 2001-03-19
FRIOR APPLICATION NUMBER: 60/191,050
FRIOR APPLICATION NUMBER: 60/191,050
FRIOR APPLICATION NUMBER: 60/191,050
FRIOR APPLICATION NUMBER: 60/254,989
FRIOR FILING DATE: 2000-12-12
FRIOR FILING DATE: 2000-12-12
FRIOR FILING DATE: 2005: 15
FRIOR FILING DATE: 2005: 15
FRIOR FILING DATE: 2005: 15
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         CURRENT APPLICATION NUMBER: US/09/692,170C
                        CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/534,639
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-10
PRIOR PILING DATE: 1998-05-10
PRIOR APPLICATION NUMBER: US 09/021,298
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR PILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VERSION 3.1
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Patent No. 6579970
GENERAL INFORMATION:
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Patent No. 6448389
GENERAL INFORMATION:
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Berencsi, Klara
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Best Local Similarity 100.00
Thes 10; Conservative
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1.FNGTH: 561
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Patent No. 6562346
GENERAL INFORMATION:
APPLICANT: Diamond, Don J.
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
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APPLICANT: Diamond, Don J
APPLICANT: Diamond, Don J
APPLICANT: Diamond, Don J
TITLE OF INVENTION: INMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN
TITLE OF INVENTION: CYTOMEGALOVIRUS
FILE REFERENCE: 1954-343
CURRENT APPLICATION NUMBER: US/09/534,639
CURRENT APPLICATION NUMBER: 09/0527
BARLIER APPLICATION NUMBER: 09/075,257
BARLIER APPLICATION NUMBER: 09/021,298
EARLIER APPLICATION NUMBER: 09/021,298
EARLIER FILING DATE: 1998-05-10
EARLIER FILING DATE: 1998-05-10
EARLIER FILING DATE: 1998-05-10
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1996-11-12
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                                                                     NAME: NEWLAND, BART G
REGISTRATION NUMBER: 31,282
REFERENCE/DOCKET NUMBER: 1954-112CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
APPLICATION NUMBER: US 08/747,488
FILING DATE: 12-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09534639 Patent No. 6251399
                                                                                                                                                                                    TELEFAX: 202-783-6031
INPORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids TYPE: amino acids STRANDEDNESS: not relevant TOPOLOGY: not relevant
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US-09-534-639-7
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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FRAGMENT TYPE: internal
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TPRVTGGGAM 10
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TYPE: PRT

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Sequence 10, Appl Sequence 31, Appl Sequence 31, Appl Sequence 41, Appl Sequence 34, Appl Sequence 34, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 33, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 34, Appl Sequence 35, Appl Sequence 36, Appl Sequence 36, Appl Sequence 37, Appl Sequence 17, Appl	
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466 28 52.8 27 1 US-0 468 28 52.8 27 1 US-0 470 28 52.8 27 1 US-0 471 28 52.8 32 3 US-0 472 28 52.8 32 3 US-0 473 28 52.8 41 2 US-0 474 28 52.8 41 2 US-0 475 28 52.8 41 2 US-0 477 28 52.8 41 2 US-0 477 28 52.8 41 2 US-0 477 28 52.8 41 2 US-0 478 28 52.8 4 US-0 479 28 52.8 88 4 US-0 470 28 52.8 88 4 US-0 471 28 52.8 88 4 US-0 472 28 52.8 88 4 US-0 473 28 52.8 88 4 US-0 474 28 52.8 88 4 US-0 475 28 52.8 100 3 US-0 488 2 28 52.8 100 3 US-0 488 2 28 52.8 100 3 US-0 489 2 8 52.8 100 3 US-0 480 2 8 52.8 100 3 US-0 481 2 8 52.8 100 3 US-0 482 2 8 52.8 100 3 US-0 484 2 8 52.8 107 2 US-0 485 2 8 52.8 107 2 US-0 486 2 8 52.8 107 2 US-0 490 2 8 52.8 107 2 US-0 491 28 52.8 107 2 US-0 492 28 52.8 107 2 US-0 493 28 52.8 107 2 US-0 494 28 52.8 107 2 US-0 495 28 52.8 107 2 US-0 496 28 52.8 107 2 US-0 497 28 52.8 107 3 US-0 498 28 52.8 107 2 US-0 499 28 52.8 107 3 US-0 499 28 52.8 107 2 US-0 490 29 5	CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0 FILING DATE: 10-FEB-1998 RAPRICATION DATA: APPLICATION NUMBER: US 0 FILING DATE: 14-OCT-1997 PRIOR APPLICATION DATA:
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US-08-568-459A-6 US-08-181-826B-6 US-09-210-28B-6 US-09-225-991A-23569 US-09-252-991A-11846 US-09-252-991A-11846 US-09-252-991A-11846 US-09-252-991A-11846 US-09-252-991A-119470 US-09-252-991A-119405 US-09-252-991A-119405 US-09-252-991A-119405 US-09-252-991A-119405 US-09-262-991A-119405	US-07-854-601-40 US-08-207-481-6 PCT-US95-02689-6 US-08-506-296B-1 US-08-566-296B-1 US-07-854-603-34 5433940-17 US-08-393-985-24
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Sequence 1885, A Sequence 2, Appli Sequence 111, Appli Sequence 111, Appli Sequence 111, Appli Sequence 110, Appli Sequence 110, Appli Sequence 29, Appli Sequence 29, Appli Sequence 2, Appli S	Sequence 25617, A Sequence 13, Appl Sequence 13, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 3, Appl Sequence 10, Appl Sequence 1, Appl Sequence 13541, A
US-09-252-991A-18853 Sequence US-09-543-681A-7306 Sequence US-09-543-691A-20577 Sequence US-09-333-208-2 Sequence US-09-333-208-2 Sequence US-09-333-254-2 Sequence US-09-28-143-75 Sequence US-09-28-143-75 Sequence US-09-205-258-143-75 Sequence US-09-205-259-1109 Sequence US-09-205-291A-18612 Sequence US-09-252-991A-1869 Sequence US-09-252-991A-1869 Sequence US-09-252-991A-1869 Sequence US-09-252-991A-1869 Sequence US-09-252-991A-1869 Sequence US-09-252-991A-19997 Sequence US-08-460-458-2 Sequence US-08-460-458-3 Sequence US-08-252-991A-29787 Sequence US-09-252-991A-29787 Sequence US-09-252-991A-29787 Sequence US-09-252-991A-29787 Sequence US-09-252-991A-29787 Sequence US-09-252-991A-29787 Sequence US-09-252-991A-2978 Sequence US-09-252-991A-21290 Sequence US-09-252-991A-21290 Sequence US-09-252-991A-21290 Sequence US-09-252-991A-21290 Sequence US-09-252-991A-21390 Sequence US-09-252-991A-21390 Sequence US-09-252-991A-235710 Sequence US-09-252-991A-23597 Sequence US-09-252-991A-2359	US-09-222-991A-25617 Sequence US-09-022-315-13 Sequence US-09-225-991A-24675 Sequence US-09-277-716-22 Sequence US-09-06-09-1461B-22 Sequence US-09-144-0000-5665 Sequence US-09-144-0000-5665 Sequence US-08-361-920-23 Sequence US-08-433-432-23 Sequence US-08-433-432-23 Sequence US-09-319-939-23 Sequence US-09-319-951B-9 Sequence US-09-74-623-70 Sequence US-09-489-039A-7605 Sequence US-09-489-039A-7605 Sequence
4 US-09-252-991A-18853 Sequence 2 US-09-433-681A-7306 Sequence 3 US-09-377-767-3 3 US-09-377-767-3 3 US-09-373-208-2 3 US-09-333-208-2 4 US-09-133-208-2 5 US-09-133-208-2 5 US-09-133-208-2 5 US-09-133-208-2 6 US-09-288-143-75 Sequence 4 US-09-205-258-1109 Sequence 5 US-09-205-258-1109 Sequence 6 US-09-205-258-1109 Sequence 6 US-09-252-991A-18612 Sequence 7 US-09-252-991A-1869 Sequence 7 US-09-252-991A-1869 Sequence 7 US-09-252-991A-19997 Sequence 7 US-09-252-991A-19997 Sequence 7 US-08-310-394A-2 7 US-08-310-394A-2 7 US-09-252-991A-29787 Sequence 7 US-08-310-394A-2 7 US-09-252-991A-29787 Sequence 7 US-08-460-455-2 7 US-09-252-991A-29787 Sequence 7 US-09-252-991A-21290 Sequence 7 US-09-252-991A-23610 Sequence 7 US-09-252-991A	4 US-09-255-991A-25617 Sequence 4 US-09-231-13 Sequence 4 US-09-277-716-22 Sequence 4 US-09-277-716-22 Sequence 4 US-09-277-716-22 Sequence 4 US-09-134-000C-565 Sequence 1 US-08-179-939-23 Sequence 1 US-08-483-432-23 Sequence 4 US-09-331-924-9 Sequence 4 US-09-724-623-70 Sequence 4 US-09-724-623-70 Sequence 4 US-09-724-623-70 Sequence 4 US-09-489-039A-7605 Sequence 4 US-09-489-039A-7605 Sequence
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OM protein - protein search, using sw model

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March 7, 2004, 13:02:32; Search time 23 Seconds (without alignments) 22.446 Million cell updates/sec

US-10-697-055-7 53 1 TPRVTGGGAM 10 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

389414 segs, 51625971 residues Searched:

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(2) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity against a biological pathway of required for proliferation, or that inhibits cellular proliferation of sequired for proliferation, or that inhibits cellular proliferation of identifying a gene required for cellular proliferation or the biological compound a activity; (1) acidlure of compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits are useful for identifying proteins or screening for homologues nucleic acids are useful for content of an organism. The antisense modeled acids required for an discovery programs or for general endecades and acids required for an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 45835; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                  06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                           21-MAR-2002; 2002WO-US009107.
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Trawick JD,
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                          WO200277183-A2.
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Sequence 768 AA;

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67.9%; Score 36; DB 6; I
75.0%; Pred. No. 1.1e+03;
tive 1; Mismatches 1;
                            6; Conservative
Query Match
Best Local Similarity
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2 PRVTGGGA 9

374 PRIPGGGA 381

AAW19212 standard; protein; 799 AA.

RESULT 50 AAW19212 ID AAW19

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Corn starch branching enzyme IIb (SBEIIb) (AAW19212) is an isoform of starch branching enzyme that shows higher rates of branching with amylopectin rather than amylose as subscrate. A cDNA inser (AAR69229) in plasmid clone pBR240 that expresses SBEIIb has been used as a starting point in the assembly of DNA constructs (see also AAR69730, AAR69736-37) designed to achieve suppression of SBEIIb expression in transgenic corn plants, and thereby to produce novel starches that have properties beneficial in food and industrial applications Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin; transgenic plant; pBB240. Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff. 67.9%; Score 36; DB 2; Length 799; 85.7%; Pred. No. 1.1e+03; Example 1; Page 50-53; 92pp; English. (DUPO) DU PONT DE NEMOURS & CO E I. Hubbard NL, Klein TM, Broglie KE; Corn starch branching enzyme IIb. 95US-0009113P. 96WO-US019678 10-SEP-1997 (first entry) WPI; 1997-341694/31. Query Match Best Local Similarity N-PSDB; AAT69729. Sequence 799 AA; 12-DEC-1996; WO9722703-A2 20-DEC-1995; 26-JUN-1997. Zea mays.

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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R, 0; Indels 1; Mismatches 7, 2004, 13:04:36 6; Conservative ||:|||| 17 PRLTGGG 23 Search completed: March Job time: 81 secs 2 PRVTGGG 8 Matches à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:732.
                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 23649; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 4; Length 261;
Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 23649.
                                                                                                                                                                                                                                                                                                                                                                                                                     PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP65988 standard; protein; 361 AA.
                              ABB65619 standard; protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.9%;
                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 TPPVMGGGAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL09722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 261 AA;
                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                          pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-2002
                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP65988;
                                                            ABB65619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 48
RESULT 47
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The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABOB1842 and ABOB1843, or a sequence exhibiting at least 10% identity or which hybridises with the sequences given in ABOB1842 and ABOB1843, or a sequence exhibiting at least 10% identity or which hybridises with the sequence exhibiting at Lagas 10% identity or which hybridises with the sequence given in ABOB1842 and ABOB1843. Also described is a polynucleotide (II) encoding a cut in ABDE5258 to ABDE6354 ligated in frame to a polynucleotide encoding a cativities, and can be used as an inhibitor of Salmonolla. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum NCC2705 (COVM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected commulk, yogurt, curd, cheese, fermented milks, milk based fermented products, ince-creams, fermented cereal based products, milk based composition conducts, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet cral supplement, dry tube feeding or wet tube feeding.

(I) is useful in DNA arrays or chips to carry out analysis of the still decided and composition of a pharmaceuticum, in the batch of a production of a pharmaceutical composition of a sphesion of the Biffidobacterium gene. ABOB1841 to ABOB1850 represent a supplement.
                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bifidobacterium related nucleotide sequences given in the Sequence fisting from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 5; Length 361;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #3438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 732; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU17911 standard; protein; 768 AA.
                                                                                                                                                                        30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                    30-JAN-2001; 2001EP-00102050.
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Best Local Similarity 87.5%
Entry 7; Conservative
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                                         Bifidobacterium longum.
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                                                                                                                                                                                                                                                                                                          WPI; 2002-668397/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 361 AA;
                                                                                   EP1227152-A1
                                                                                                                               31-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU17911;
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Bacillus anthracis.

1 TPRVTGGG 8

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74 TPRLNGGG 81

RESULT 46

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed can be useful in gene therapy techniques to restore normal cativity of (II) as useful in gene therapy techniques to restore normal cativity of (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, formsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABG00010-ABG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MPO at the printed specification, but was obtained in electronic format directly from MPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%; Score 36; DB 4; Length 98; 75.0%; Pred. No. 1.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 32426; 103pp; English.
                                                                                                                                                                                                                                   Novel human diagnostic protein #2058.
                                                                                                      ABG02067 standard; protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217
                                                                                                                                                                                         13-FEB-2002 (first entry)
96 TPRVFGGG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS66254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001.
                                                                                                                                                   ABG02067;
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                                                              RESULT 45
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic partent did not annear in the printing result in the printing in the printing and the printing and products dependent on DNA and amino acid sequences of the invention. Note: The sequence other this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 45547; 103pp; English,
                                                                                                                     Novel human diagnostic protein #15179.
ABG15188 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 77.0.
                                                                               18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                                                                                                                                          Homo sapiens,
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                                       ABG15188;
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0; Gaps

6; Conservative

Matches

1 TPRVTGGG 8

:||| |||| 53 SPRVHGGGA 61

ABM55760 RESULT

ABM55760 standard; protein; 103 AA.

ABM55760;

(first entry) 20-0CT-2003 Propionibacterium acnes predicted ORF-encoded polypeptide #20436.

Acme vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Carter D; Maisonneuve JL; Jones R, Carte Bhatia A, Benson DR, W, Persing DH, S, Lodes MJ, Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J; Skeiky YAW, ng S, Jen S Mitcham JL,

WPI; 2003-381789/36. N-PSDB; ACF64530. New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 20436; 1481pp; English

The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

concoding a Propionibacterium acnes protein. The invention also relates to encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a colymucleotide of the invention; and propertied and invention; and propertied of the invention; and invention; and an isolated T cell population comprising T cells prepared to invention; at this method; a vaccine composition (comprising P. acnes polypeptides, polymorptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymptide; a method and xit continuing the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a continuing the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a continuing the presence or absence of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the polymorphic or antigen propertied for diagnosing, preventing or treating acnes to protein. The p. acnes polypeptides, polymorphicides, in the polymorphic or antigen-presenting cells that express the polymorphic or antigen-presenting cells in a necestary or for stimulating an immune response specific for a P. acnes protein. The polymorphic can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents applyapented predicted to be encoded by an ORF (open creating frame) contained within the P. acnes polymorphic or active contained within the P. acnes polymorphic or the printed specification, but was obtained in electronic format directly contained with a polymorphic or and the printed specification, but was obtained in electronic format directly contained between the printed specification, but seed as processed to the printed processed to the printed processe

Sequence 103 AA;

DB 6; Length 103; 69.8%; Score 37;

ö Gaps . 0 1; Indels ed. No. 87; Mismatches Pred. No. 77.8%; 7; Conservative Best Local Similarity Matches

σ 1 TPRVTGGGA ਨੇ

53 SPRVHGGGA 61

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ABR'01485 standard; protein; 214 AA. **ABR01485**

ABR01485;

16-APR-2003

Human anti-TIMP-1 antibody light chain #26.

matrix metalloprotease; MWP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;

idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

ното варіепв.

WO200286085-A2.

31-OCT-2002.

24-APR-2002; 2002WO-US012801

24-APR-2001; 2001US-0285683P

(FARB) BAYER CORP. (MORP-) MORPHOSYS AG.

Krebs B; Hirth-Dietrich C, Kraft S, Pan C, Knorr AM, Schauer M,

WPI; 2003-129114/12. N-PSDB; ABZ74842 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung cancer.

Claim 21; Page 135-136; 228pp; English.

The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and inbody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP contains a variable heavy chain (VHC) DR3 region and a cariable light chain (VLC) DR3 region. An antibody preparation of the continuity of a TIMP-1 it is especially useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, and contary syndrome, lupus nebritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 is elevated. The sequences shown in ABR01460-ABR01501 represent the light chain regions of a human anti-TIMP-1 antibody of the invention

Sequence 214 AA;

Gaps .. 0 Length 214; Score 3,, Pred. No. 1.9e+02; 69.8%; Score 37; DB 6; 87.5%; Pred. No. 1.9e+02 0; Mismatches Query Match
Best Local Similarity 87.5³
Matches 7; Conservative

0;

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990S-0155659P.
990S-0156458P.
990S-0156596P.
990S-0157117P.
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99US-0151438P.
99US-0151930P.
99US-0152363P.
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990S-0154739P.
990S-0155139P.
990S-0155486P.
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99US-0161920P.
99US-0147935P.
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99US-0148319P.
99US-0148361P.
99US-0148655P.
99US-0148684P.
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99US-0150884P.
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99US-0160741P.
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                                                                         99US-0149723P
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                                                           99US-0149426P
                                                                  99US-0149722P
                                                                                        99US-0149902P
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06.0CT-1999
08.0CT-1999
13.0CT-1999
13.0CT-1999
13.0CT-1999
14.0CT-1999
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14.0CT-1999
14.0CT-1999
14.0CT-1999
14.0CT-1999
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                            13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                      10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
                                                                                              23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
                                                                                20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                     18-0CT-1999)
21-0CT-1999)
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21-0CT-1999,
                                                                           20-AUG-1999
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87.5%;
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                                Gaps
                               ;
0
71.7%; Score 38; DB 3; Length 401;
                               1; Indels
              Pred. No. 2.5e+02;
                             0; Mismatches
              Best Local Similarity 87.5
Matches 7; Conservative
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                              Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                    Propionibacterium acnes immunogenic protein #20137.
                                             AAU59241 standard; protein; 103 AA.
                                                                                                                                                                                                                                       21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                       20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                      L'maisonneuve J, Zhang Y,
                                                                                   (first entry)
                                                                                                                                                                   Propionibacterium acnes.
80 resvrede 87
                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS59601.
                                                                                   27-FEB-2002
                                                                                                                                                                                                      01-NOV-2001.
                            RESULT 42
                                      AAU59241
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Propionibacterium acmes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 20436; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypercosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies only peptides may be used as antigens in the production of antibodies of the refore treat P. acnes proteins. The antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for the print of the printed specification, but was ftp.wipo.int/pub/published_pct_sequences

Sequence 103 AA;

Gaps . 0 h Similarity 77.8%; Score 37; DB 4; Length 103; Similarity 77.8%; Pred. No. 87; 7; Conservative 1; Mismatches 1; Indels Best_Local Similarity Matches 7; Conservat Query Match

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1 TPRVTGGG 8

us-10-697-055-7.rag

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9905-013847P.
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9905-0139452P.
9905-0139453P.
9905-0139455P.
9905-0139455P.
9905-0139456P.
9905-0139456P.
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9905-0139458P.
9905-0139463P.
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9905-014085P.
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9905-014133P.
9905-014332P.
9905-014332P.
9905-014333P.
9905-0144332P.
9905-0144333P.
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03-AUG-1999;
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                                                                                                                                                                        Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                  Gaps
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                 Ouery Match 71.7%; Score 38; DB 3; Length 401; Best Local Similarity 87.5%; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 64199.
                                                                                                          AAG50642 standard; protein; 401 AA.
                                                                                                                                                                                                                                                                                990S-0123180P-
990S-012548P-
990S-012548P-
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990S-012678EP-
990S-0128714P-
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990S-013248P-
990S-013248P-
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990S-013421P-
990S-013431P-
990S-0135529P-
990S-0137328P-
   PR 29-OCT-1999; 99US-0162142P.
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                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                  80 TPSVTGGG 87
                                                 1 TPRVTGGG 8
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21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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14-MAY-1999;
18-MAY-1999;
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                                                                                                                           AAG50642;
                                                                                            RESULT 41
                                                                                                     AAG50642
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UUS-0136392P UUS-0137722P UUS-0137528P UUS-0137524P UUS-0137524P UUS-0137624P UUS-0137624P UUS-0137624P UUS-0137624P UUS-0133453P UUS-0133453P UUS-0133453P UUS-0133453P UUS-0133453P UUS-0133453P	105.0139457 105.0139459 106.0139459 107.0139460 108.0139461 108.0139461 108.0139461 108.0139461 108.0139461 108.0139461 108.0140821 108.0140821 108.014287 108.014287 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297 108.01428297	990S-0144086P 990S-0144332P 990S-0144333P 990S-0144333P 990S-0144334P 990S-0144335P 990S-0144335P 990S-0144332P 990S-0144832P 990S-0144814P 990S-014508F 990S-014508F 990S-014508P 990S-014508P 990S-014508P 990S-014519P 990S-014513P 990S-014513P 990S-014513P 990S-014531P 990S-014531P 990S-014531P 990S-014531P 990S-014531P 990S-014531P 990S-014531P
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UUS-0147204P UUS-0147302P UUS-0147302P UUS-0147260P UUS-0147404P UUS-0147935P UUS-0147935P UUS-0148841P UUS-0148841P UUS-0148841P UUS-0148841P UUS-0148841P UUS-0148841P	990'S-0149'722P. 990'S-0149'723P. 990'S-0149'922P. 990'S-01499'02P. 990'S-01499'30P. 990'S-015086R. 990'S-0151066P. 990'S-0151066P. 990'S-0151080P. 990'S-0151080P. 990'S-0151080P. 990'S-015130P. 990'S-015133P. 990'S-01533P. 990'S-01533P. 990'S-0154'39P. 990'S-0154'39P. 990'S-0154'39P. 990'S-0154'779P.	9US-0155659P 9US-0156596P 9US-0156564B 9US-0157753P 9US-0157753P 9US-0158293P 9US-0159294P 9US-0159294P 9US-0159294P 9US-0159294P 9US-0159294P 9US-0159294P 9US-0159294P	905-01607689 905-01607689 905-01607089 905-01608159 905-01608159 905-01609809 905-01614049 905-01614069 905-01614069 905-01614069 905-01614069 905-01614069 905-01614069
1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999 1-Aug-1999	20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AU	4.5EP-1999 9.5SEP-1999 9.5SEP-1999 4.0CT-1999 7.0CT-1999	1-001-1999 1-007-1999 1-007-1999 1-007-1999 2-007-1999 5-007-1999 5-007-1999 6-007-1999 8-007-1999
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and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to dervironmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally coccurring CCP substrates. The polynucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence represents a CCP protein of
                                                                                                                                                                                                                                                                                                                                                                                      the invention
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Sequence 383 AA;

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ö
                               Gaps
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0
         Score 38; DB 5; Length 383; Pred. No. 2.3e+02; 0; Mismatches 1; Indels
         71.78;
87.58;
Query Match
Best Local Similarity 87.5
Trace 7; Conservative
                                                      à
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RESULT 39

ADD30432 standard; protein; 383 AA. ADD30432

ADD30432;

(first entry) 15-JAN-2004 Plant yield-related protein from clone G2373.

transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.

Arabidopsis thaliana.

WO2003013227-A2.

20-FEB-2003.

09-AUG-2002; 2002WO-US025805.

19-NOV-2001; 2001US-0336049P. 11-DEC-2001; 2001US-0338692P. 09-AUG-2001; 2001US-0310847P. 14-JUN-2002; 2002US-00171468. (MEND-) MENDEL BIOTECHNOLOGY INC

Yu G, Dubell AT, Heard JE; Adam LJ, Dubell Arr TL, Creelman RA, Reuber TL, Riechmann JL, Jiang C, Ratcliffe O, Pilgrim ML, J Broun PE;

2003-248221/24. WPI; 2003-248221/ N-PSDB; ADD30431. New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate

Disclosure; SEQ ID NO 461; 454pp; English.

The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant,

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such as an alteration in a plant growth characteristic, e.g. growth rate,
                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
        germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polymucleotides and also be used in boinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the proteins of the invention.
                                                                                                                         Gaps
                                                                                                                        0;
                                                                                                71.7%; Score 38; DB 7; Length 383; 87.5%; Pred. No. 2.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 13672.
                                                                                                                                                                                                                            AAG13980 standard; protein; 401 AA.
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99US-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
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99US-0132407P.
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99US-0134218P.
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                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                             termination sequence
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                      Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                    62 TPSVTGGG 69
                                                                                                                                                1 TPRVTGGG 8
                                                                             Sequence 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1999;
30-APR-1999;
04-MAY-1999;
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01-APR-1999;
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The invention relates to a novel cell cycle protein (CCP) and the polymorleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP modelet and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat clastoctarised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or berrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or polymorleotide are useful as herbicides or plant growth regulators. The polymorleotide is useful for modifying cell fate, plant development, of cell civile or production, plants of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, nobel function, dwarfism in plants, initiation and root initiation and/or development, notelle function, dwarfism in plants, sensessice or seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen.
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                                                                                                                                                                       Gaps
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                                                                                                                              71.7%; Score 38; DB 3; Length 383; 87.5%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                         AAU72500 standard; protein; 383 AA.
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           990S-0161361P.
990S-0161920P.
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N-PSDB; AAS96290.
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                                                                                                          71.7%; Score 38; DB 3; I
llarity 87.5%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 1;
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les 7; Conserv
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Pred. No. 2e+02;
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99US-01593310P.
99US-01593310P.
99US-01596317P.
99US-01596317P.
99US-0160767P.
99US-0160767P.
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99US-0161768P.
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                                                                                                                                                                                                                    71.78;
87.58;
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                                                                                                                                                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                                                                                           Local Similarity 87.5 es 7; Conservative
                                                                                                                                                                                                                                                            10 TPSVTGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                  1 TPRVTGGG 8
13-0CT-1999;

13-0CT-1999;

14-0CT-1999;

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14-0CT-1999;

14-0CT-1999;

14-0CT-1999;

12-0CT-1999;

21-0CT-1999;

21-0CT-1999;

22-0CT-1999;

22-0CT-1999;

22-0CT-1999;

23-0CT-1999;

25-0CT-1999;

26-0CT-1999;

26-0CT-1999;
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05-MAR-1999;
03-MAR-1999;
23-WAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
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                                                                                                                                                                                                                                                                                                                       AAG13982;
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Matches
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99US - 013244 079
99US - 013248 4P.
99US - 013248 8P.
99US - 013248 8P.
99US - 013248 8P.
99US - 01342 5P.
99US - 01342 18P.
99US - 01342 18P.
99US - 01342 18P.
99US - 01342 1P.
99US - 01342 1P.
99US - 01342 1P.
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99US - 01356 2P.
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99US - 01375 0P.
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99US-0139458P.
99US-0139461P.
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99US-0140695P.
99US-0140991P.
99US-0141287P.
99US-0141842P.
99US-014205-99US-014205P.
99US-014205-99US-014205P.
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99US-0144085P-
99US-0144332P-
99US-0144331P-
99US-0144334P-
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99US-0143542P.
99US-0143624P.
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US-0128234P US-012814P US-0129845P US-0129845P US-0130649P US-0130891P US-013240P US-013240P US-013240P US-013240P US-013240P	990G-0134218F 990G-0134219F 990G-0134219F 990G-0134341F 990G-0134941F 990G-0135353F 990G-0135353F 990G-0135353F 990G-0135353F 990G-0135353F 990G-0135622F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0137528F 990G-0139458F 990G-0139458F 990G-0139458F 990G-0139458F 990G-0139458F	1015 - 01397631 1018 - 01398931 1018 - 0140354 1018 - 0140354 1018 - 01406925 1018 - 01406925 1018 - 01406925 1018 - 0141287 1018 - 0141287 1018 - 0142395 1018 - 0142395 1018 - 0142395 1018 - 0142395 1018 - 0143365 1018 - 0144085 1018 - 01444085 1018 - 01443331
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hillammancory disorder; infection; hormonal disorder; metabolic disorder;
neurological disorder; gastrointestinal disorder; transport disorder;
connective tissue disorder; drug screening; proteome analysis;
gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
disease model; toxicological testing; transcript imaging;
intracellular signalling.
involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                   Length 197;
                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                   2e+02;
                                                                                                                                                                                                    71.7%; Score 38; DB 4;
85.7%; Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DITHP intracellular signalling protein.
                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     ABR41269 standard; protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
17-UUN-2001; 2001US-0299428P.
20-UUN-2001; 2001US-0299776P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2002; 2002WO-US010056.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0300001P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                               PRVTGGG 8
                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                           3 PRITGGG 9
                                                                                                                                                                        Sequence 197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                   ABR41269;
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                       RESULT 33
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The invention relates to novel human diagnostic and therapeutic polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded portucines DITHP; ARR4118-ARR41812). The invention also relates to polymucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and comparison comprising dithp mucleic acid sequences; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; antibodies specific for DITHP proteins; methods of sessing the toxicity of test compounds using a dithp hybridisation of probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell compounds with a wide variety of conditions including cancer and other cell grobe. Dithp nucleic acid sequences and DITHP proteins may be used in the probe. Dithp nucleic acid sequences and DITHP proteins may be used in the proliferative disorders; autoimmune or inflammatory disorders; metabolic confiscative disorders; mucrological disorders; promerial disorders; metabolic disorders; and connective tissue disorders; metabolic disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP conteins can additionally useful in somatic or garmline gene therapy of the disorders additionally useful in somatic or garmline gene therapy of the disorders concell type and to induce antibodies. The dithp nucleic acids at source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence expresents a DITHP protein was obtained in electronic format cigaralling activity. Note: The sequence data for this parent did not form signalling activity. Note: The sequence additionally protein and protein additionally but was obtained in electronic formating ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 38; DB 6; Length 270; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                Claim 27; SEQ ID NO 804; 591pp; English.
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99US-0123548P.
99US-0125788P.
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99US-0126785P.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 TPRVTGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPRVTGG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033405-A2
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99US-0127462P

01-APR-1999;

Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Geretin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;

Dufour GE, Hillman JL Daughtery SC, Dam TC,

Peralta CH,

Flores V,

WPI; 2003-129518/12.

N-PSDB; ACC46211.

us-10-697-055-7.rag

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HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore; genital herpes; chickenpox; shingles.
                                                                                                                                       New antiviral agent disrupting binding of VP22 to VP16 or gB - useful for treating infections caused by herpes simplex, e.g. cold sores and chicken
                                                                                                                                                                                                          The present sequence is a herpes simplex virus (HSV) truncated tegument protein VP22 derived peptide. VP22 was used in the preparation of a novel mativiral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, chickenpox and
                                                                                                                                                                                                                                                                                                                      71.7%; Score 38; DB 2; Length 19; 100.0%; Pred. No. 9.8; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus truncated tegument protein VP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "residues 158-267 of VP22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rixon HWM;
                                                                                          Rixon HWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "histidine tag motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132. .144
/note= "epitope tag motif"
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                                                                                         Hope RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47195 standard; peptide; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus unknown type.
                                                                                                                                                                                          Example; Page 25; 75pp; English.
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                    97WO-GB002036.
                                            96GB-00015726
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                                                                   (MEDI-) MEDICAL RES COUNCIL.
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                                                                                             Mclaughlan J, Mcgeoch DJ,
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/note= "r
                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                   WPI; 1998-130696/12.
                                                                                                                                                                                                                                                                                                                                                                                               13 TPRVTGG 19
                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                       1 TPRVTGG 7
                                                                                                                                                                                                                                                                                                 Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1997;
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                      28-JUL-1997;
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                                              26-JUL-1996;
05-FEB-1998.
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       New antiviral agent disrupting binding of VP22 to VP16 or gB - useful for treating infections caused by herpes simplex, e.g. cold sores and chicken
                                                                                                                   The present sequence is the herpes simplex virus (HSV) truncated tegument
                                                                                                                                                                       рe
                                                                                                                                protein VP22. VP22 was used in the preparation of a novel antiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, chickenpox and shingles
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                  Length 144;
                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                DB 2;
83;
                                                                                                                                                                                                                                                                71.7%; Score 38; DB 100.0%; Pred. No. 83; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 47092; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #16724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG16733 standard; protein; 197 AA.
                                                                                    Example; Page 52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                           138 TPRVTGG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                         1 TPRVTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS80920
                                                                                                                                                                                                                                  Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
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Gaps ô

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein comprising a lipid globule targeting sequence consisting of a heparitis C virus core protein, useful for targeting a protein of interest to lipid globules which are subsequently secreted into animal milk.
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               Gaps
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                                                                                                                                                                                                                                                             Hepatitis C; targeted protein production; core protein; linker.
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Pred. No. 1.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                  Chimaeric hepatitis C virus core protein linker peptide.
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                                                                                                                                              AAB01253 standard; protein; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 42; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           98GB-00025953.
                                                                                                                                                                                                                                                                                                                                                                               99WO-GB003898.
77.8%;
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Best Local Similarity luv...
7; Conservative
                Conservative
                                                                       332 PRVPGGGAL 340
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                                            2 PRVTGGGAM 10
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 Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                       WO200031127-A2.
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                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1999;
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                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                          AAB01253;
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                                                                                                                 RESULT 28
                                                                                                                                  AAB01253
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This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino acid sequence of the antigen into protein fragments (II) of at least 9 amino acids whereby adjacent or neighbouring fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension comprising (II) in a single culture vessel. The method is used to immunoserializate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in vivo or in vitro immuno-stimulation of mammalian, more preferably human T imphocytes, where the stimulated T lymphocytes are expanded and can be transfused into a partient. ABBS654-ABB8681 represent fragments of the human cycomegalovirus IE1 and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore; genital herpes; chickenpox; shingles.
                                                                                                                                                                                                                                                                                                                                                                              Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
          Antigen-specific stimulation, T-lymphocyte, CD8 stimulation, pp65; CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSV truncated tegument protein VP22 derived peptide J.
                                                                                                                                                                                                                                                                                                        Reinke P, Faulhaber N, Surel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW47205 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       simplex virus unknown type.
                                                                                                                                                                                       L7-FEB-2001; 2001WO-EP001773.
                                                                                                                                                                                                                             22-FEB-2000; 2000DE-01009341
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 2; 85pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                        Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                            WPI; 2001-557718/62.
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                                                                                                                                                                                                                                                                                                        Kern F, Volk H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                            WO200163286-A2.
                                                                                                                                                                                                                                                                   (KERN/) KERN
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X B X S S X X X X B X B X B X X X X X B
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and there is no native expression of endogenous CAP1 is a serine protease
and there is no native expression of endogenous CAP1 gene. Transgenic
mice with a heterologous disruption in the CAP1 gene exhibit an increased
susceptibility to seizures which are similar to epilepsy. Disclosed is a
method for producing the transgenic mouse with a disruption in the CAP1
gene which contains a targeting construct comprising a first or second
polynucleotide sequence homologous to at least a first or second portion,
respectively, of the CAP1 gene and a selectable marker. Also disclosed
are methods for identifying an agent that modulates susceptibility to
seizure or the phenotype, for identifying a potential therapeutic agent
correction appliepsy, for evaluating a potential therapeutic agent
capable of affecting a condition associated with a mutation in a CAP1
gene (e.g. a CAP1 agonist) and for determining whether an agent modulates
a CAP1 serine protease. The transgenic mouse, comprising a disruption in
a CAP1 gene, is useful for preparing a pharmaceutical composition for
treating epilepsy. The sequence presented is the mouse CAP1 protein
                                                                                                          The invention discloses a new transgenic mouse comprising a disruption in
           New transgenic mouse comprising a disruption in a CAP1 gene, useful for preparing a pharmaceutical composition for treating epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the Eimeria antigen Eam200. It is useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria; coccidiosis; chickens; fowl; vaccines; immunise; vaccinate; immunoassay; test; detection; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope(s) of Eimeria antigens - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.6%; Score 39; DB 6; Length 339; 75.0%; Pred. No. 1.4e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vermeulen AN;
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anticoccidiosis vaccines and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR29924 standard; protein; 447 AA.
                                                                    Disclosure; Fig 2; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91EP-00201523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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(ALKU ) AKZO NOBEL NV
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N-PSDB; AAQ31997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1992;
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28-APR-1993
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The Bimeria acervulina 200 kD antigen, recombinant vector viruses or host cells are used to produce vaccines to protect avians against coccidiosis particularly chickens. The waccine can also contain immunogens related to other pathogens found in poultry or may contain nucleic acid encoding them e.g. antigens of Marek's Disease virus, Newcastle Disease virus, Chicken Anaemia Agent, Reo virus, Infectious Bursal Disease virus, Chicken Anaemia Agent, Reo virus, E. Coli or other Eimeria species to produce a multivalent vaccine. The nucleic acids are useful as hybridisation probes to isolate sequences encoding functional variant proteins e.g. from tissues or a cDNA library from a specific Bimeria strain. The nucleic acid is additionally used in test kits for diagnosis of Eimeria cleic infections and in immunoassays. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins or fragments having immunogenic determinants of Eimeria antigens, nucleic acid, recombinant vector, host cell and antibody - used as vaccine against coccidiosis in avians e.g. chickens.
vaccine for protecting chickens against coccidiosis. It is also useful an immunoassay reagent. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                             Gaps
                                                                                                                                             ó
                                                                                                          Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eimeria acervulina; vaccine; coccidiosis; poultry; avian;
                                                                                                      / Match 73.6%; Score 39; DB 2; Length 447 Local Similarity 77.8%; Pred. No. 1.8e+02; nes 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vermeulen AN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eimeria acervulina 200kD antigen fragment.
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                                                                                                                                                                                                                                                                                                      AAW58567 standard; protein; 447 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97EP-00203394
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92EP-00201673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant virus vector.
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                                                                                                                                                                                                                   332 PRVPGGGAL 340
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                                                                           Sequence 447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                                                          AAW58567;
                                                                                                              Query Match
       vaccine
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                      RESULT 27
                                                                                                                                                                                                                                                                                           AAW58567
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Length 447;

DB 2;

73.6%; Score 39;

Sequence 447 AA;

Query Match

Glaser P, Frangeul L, Kunst F, Danchin A;

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the geneme of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the colypoptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that corresponse or sensitivity to toxins and antibiotics produced by P. capponse or sensitivity to toxins and antibiotics produced by P. combinant production of the proteins, particularly toxins and crecombinant vectors containing the genes and Ab are also useful crecombinant production singettion by bacteria or fungithat are sensitive to P. luminescens-encoded toxins or antibiotics) and as compensationes. Other uses of the genes and the proteins are very constructions. This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virucide, immunostimulant; cytotoxic T-lymphocyte, CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1; IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
                                                                                                                                                                                                                                                                                                     Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus CTL epitope peptide SEQ ID No 30.
                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 2842; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37972 standard; peptide; 9 AA.
                                                                                                                                         INSP ) INST PASTEUR.

CNRS ) CNRS CENT NAT RECH SCI.
                                                        07-FEB-2002; 2002WO-IB003040.
                                                                                                   07-FEB-2001; 2001FR-00001659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                      Taourit S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PRVTGGGA 9
                                                                                                                                                                                                                                                                  WPI; 2003-148459/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransplantation.
                                                                                                                                                                                                                         Buchrieser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2003
                   28-NOV-2002.
                                                                                                                                                                                                        Duchaud E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ37972
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The invention relates to a novel isolated peptide comprising one or more cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, IG2, US2, US3, US6, US11 or UL18. The peptide comprises a sequence of about 9-20 contiguous amino acids of treating cytomegalovirus infection in humans, and in monitoring immune responses in various clinical settings (e.g. transplantation or pregnancy). This sequence represents a human cytomegalovirus CTL epitope peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, enzyme; transgenic; channel activating protease 1; CAP1; serine protease; seizure; epilepsy; therapeutic; agonist; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                     for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.
                                                                                                                                                                                                                                                                                                                                                      New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.4%; Score 41; DB 6; Length 9;
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse channel activating protease 1 (CAP1) protein.
                                                                                                                                                        (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                             Walker SJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG72018 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 105; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2001US-0280509P.
08-AUG-2001; 2001US-0311055P.
28-MAR-2002; 2002US-00109616.
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                                                                                      26-JUN-2001; 2001AU-00005931.
                           26-JUN-2002; 2002WO-AU000829
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Les 8; Conservative
                                                                                                                                                                                                                             Elkington RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DELT-) DELTAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058636/05.
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                                                                                                                                                                                                                                                                                        WPI; 2003-300379/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2003
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                                                                                                                                                                                                                             Khanna R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG72018;
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Matches
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Gaps

81.1%; Score 43; DB 6; Length 172; 100.0%; Pred. No. 14; 0; Mismatches 0; Indels

(first entry)

03-JAN-2003.

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us-10-697-055-7.rag

22-MAY-2003 (first entry)

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1 TPRVTGGGA

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The invention relates to a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal:

(a) an antigen in the form of a polypeptide; (b) a vector comprising a nucleic acid encoding the antigen; or (c) a non-peptide antigen. The method is useful for treating and/or sustaining CTL response in a mammal. This is particularly useful for treating a mammal having a malignant tumnour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious disease (e.g. hepatifits, acquired immune deficiency syndrome (AIDS), malaria, measles or tuberculosis), or in an animal having a predisposition to these diseases. The mammal may be dogs, cats, mice, cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-ABG80119 represent viral epitopes on major histocompatibility complex (MHC) class I molecules, used in the method of the invention
                                                                                                                                                                                          Major histocompatibility complex; MHC; MHC class I molecule; virus; epitope; cytotoxic I lymphocyte response; CTL response; lymphatic system; antigen; immunogenic; malignant tumnor; carcinoma; melanoma; leukaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis; acquired immune deficiency syndrome; ALDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing or sustaining immunological cytotoxic T lymphocyte response in a mammal, useful for treating a mammal with malignant tumor or infectious disease, by directly administering an antigen to the lymphatic system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%; Score 46; DB 5; Length 15; 90.0%; Pred. No. 0.31; tive 0; Mismatches 1; Indels
                                                                                                                                                          MHC class I molecule, viral epitope #148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 22; 73pp; English.
                                  ABG79900 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-2001; 2001US-00776232.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2002; 2002WO-US002033
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kundig TM, Simard JJL;
                                                                                                                                                                                                                                                                                                                          Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-657506/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                   WO200262368-A2.
                                                                                                                   15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2002.
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                                                                             ABG79900;
RESULT 21
                     ABG79900
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                  83.0%; Score 44; DB 6; Length 11; 100.0%; Pred. No. 0.5;
                                    0; Indels
                                                                                                                                                                                     Photorhabdus luminescens protein sequence #2842.
                      bs.v..
100.0%; Prea. vv..
-ive 0; Mismatches
                                                                                                                           ABM69745 standard; protein; 172 AA.
                                                                                                                                                                   (first entry)
                                      8; Conservative
                                                                                                                                                                                                                                                         Photorhabdus luminescens
                                                        1 TPRVTGGG 8
                        Best Local Similarity
Matches 8; Conser
Sequence 11 AA;
                                                                                                                                                                                                                                       whooping cough.
                                                                                                                                                                                                                                                                             WO200294867-A2
                                                                                                                                                                   20-NOV-2003
                                                                                                                                               ABM69745;
                   Query Match
                                                                                                          RESULT 23
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Gape .; 0

9; Conservative

1 TPRVTGGGAM 10 TPRVTXGGAM 12 ABJ37950 standard; peptide; 11 AA.

RESULT 22
ABJ37950
ID ABJ37
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                                                                                                                Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1; IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                             Human cytomegalovirus CTL epitope peptide SEQ ID No 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 105; Page 133; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khanna R, Elkington RA, Walker SJ
                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001; 2001AU-00005931.
                                                                                                                                                                                                                                                                                                                                                      26-JUN-2002; 2002WO-AU000829
                                                                                                                                                                                                                          Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-300379/29.
                                                                                                                                                                                        transplantation.
                                                                                                                                                                                                                                                                      WO2003000720-A1.
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Sun Mar

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The invention relates to immunologically active peptides, and functional variants thereof, capable of eliciting a cellular immune response to human cytorhegalovitus (HCMV) in humans. The peptides are capable of directing human cytotoxic I lymphocytes (CTL) to recognise and lyse human call infected with HCMV. Such immunologically active peptides, in association with an major histocompatibility complex (HHC) class I (inactive) HCMV infection. Vaccines of individuals having a latent (inactive) HCMV infection. Vaccines comprising these peptides are useful for activating CTLs and CTL precursors (CTLp), particularly for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The peptides may be used in an assay for determining the degree of immunostimulation caused by HCMV. The peptides may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           distinguishing individuals who are seropositive from those who have not been exposed to HCMV (seronegative individuals). The present peptide sequence is a cytotoxic epitope variant from human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides that are immunogenic epitopes of the human cytomegalovirus (CMV), useful for activating cytotoxic T lymphocytes (CTL) or CTL precursors to elicit an immune response against human CMV by normal or immunodeficient subjects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus, HCMV, cytotoxic epitope, infection, vaccine, cytotoxic T lymphocyte, CTL, CTL precursor; CTLp, Class I antigen, emajor histocompatibility Complex, MHC, cellular immune response; CTL activator; 
                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus (HCMV) cytotoxic epitope variant #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                       AAE05432 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 7; 17pp; English.
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97US-00950064.
98US-00021298.
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-431950/46.
TPRVTGGGA
                                                            TPRVTGGGA
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14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                        24-SEP-2001
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                                                                                                                                                                                                                                                                                       AAE05432;
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The invention relates to immunogenic peptides derived from human cytomegalovirus (HCMV) which are recognised by human cytotoxic T-Iymphocytes (CTL). The invention also discloses a vaccine against HCMV comprising one of the peptides, and a pharmaceutically acceptable carrier, a cellular vaccine against HCMV comprising antigen presenting cells that have been treated in vitro so that they express the peptide, and a recombinant viral vector vaccine expressing a gene encoding the peptide. The vaccine is used to modulate the immune response to human cytomegalovirus infection. HCMV is implicated in a number of diseases and conditions including restenosis after coronary angioplasty, morbidity/mortality in AIDS (acquired immunodeficiency syndrome) patients, viral retinitis leading to blindness, encephalitis, enterities, morbidity/mortality in AIDS (acquired immunodeficiency syndrome) carcomal and post-bone marrow transplant complications. The present sarcomal and post-bone marrow transplant complications. The present services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic peptides useful as a vaccination against cytomegalovirus infection, comprises epitopes of human cytomegalovirus which are recognized by human cytotoxic T-lymphocytes.
                                                                                                                                                                                                                                                                           Immunogenic epitope; pp65; cytotoxic T cell; CTL; HCMV; vaccine; virucide; restenosis; coronary angioplasty; morbidity; mortality; AIDS; acquirted immunodeficiency syndrome; viral retinitis; blindness; encephalitis; enteritis; monucleosis; interstitial pneumonia; malignancy; Karposi's sarcoma; post-bone marrow transplant complication.
                                                                                                                                                                                                                                            Human cytomegalovirus pp65 protein based immunogenic epitope #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%; Score 48; DB 5; Length 10; 100.0%; Pred. No. 0.091; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                AAU10827 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2000; 2000US-00534639.
20-OCT-2000; 2000US-00692170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001; 2001WO-US008576.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (cfry ) ciry of HOPE.
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                                   TPRVTGGGA
1 TPRVTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200172782-A2
                                                                                                                                                                                                          14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Gaps

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100.0%; Pred. ...

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Best Local Similarity

Matches

1 TPRVTGGGA 9

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Gaps

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Best Local Similarity Matches 9; Conserv

Human cytomegalovirus immunogenic peptide SEQ ID NO:8.

(first entry)

20-OCT-2000

AAB12413;

AAB12413 standard; peptide; 10 AA.

RESULT 18

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cytocoxic T lymphocytes. The antigen presenting cells primed with the IAPs can be used as diagnostic reagents to detect immunostimulation by HCMV. They can also detect active HCMV infection or exposure to HCMV. HCMV can cause opportunistic infections resulting in a variety of complications in, e.g. immunosuppressed patients. The IAP vaccines impart immunity to bone marrow transplant recipients, solid organ recipients, heart patients, AIDS patients or women of child-bearing years, without the need for ex vivo expansion of HCMV-specific cytocoxic T lymphocytes (which requires sophisticated laboratory setup and is highly labor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes immunologically active peptides (IAPS) capable of eliciting a cellular immune response to human cytomegalovirus (hCMY). The IAP can be used in a (cellular) vaccine to augment the immune system response to HCMV, or to provide immunity against HCMV. The IAP (cellular) vaccine can also protect an individual having a latent HCMV infection from reactivation. An antigen presenting cell can be used to determine the presence or absence of HCMV-infected Ilymphocytes. The viral vector containing IAP encoding DNA can also be used to provide immunity against HCMV. The IAP can be used to prepare HCMV-reactive human
                                                                                                                                                                         Human cytomegalovirus; hCWV; immunologically active peptide; vaccine; immune response; cytotoxic T lymphocyte; CTL; immunostimulation; infection; immunosuppression; bone marrow transplant; solid organ; heart;
                                                                                                                                     Immunogenic peptide cytotoxic I lymphocyte epitope SEQ ID NO:8 of hCMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide cytotoxic T lymphocyte epitopes of human
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100.0%; Pred. No. 0.091;
:ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       /label= Leu, Met, Phe
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                               AAY09315 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 49; 64pp; English.
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98US-00021298.
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Best Local Similarity 100..
Thes 9; Conservative
                                                                                                        08-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diamond DJ, York J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-277590/23.
                                                                                                                                                                                                                                                                           Human herpesvirus 5.
                                                                                                                                                                                                                                                                                                                                                      Misc-difference 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                             WO9919349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-0CT-1997;
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                                                                                                                                                                                                                                                                                               Synthetic
                                                                      AAY09315;
RESULT 17
                   AAY0931
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The present invention describes a cellular vaccine (I), which elicits a mHC Class I cellular immune response to human cytomegalovirus (HCWV), and comprises a peptide selected from (i) - (V), provided that (i) is not another peptide (vi): (i) Ann Xaal Val Pro Met Val Pro Kaa2; (ii) Tyr Caa3 (Glu His Pro Thr Pro Arg Val Pro Met Val Pro Lys Asa (V) Phe Ca Thr Lys Asp Val Ala Leu, where Xaal = Leu, Ile, Met, Thr or Lys Asp Val Ala Leu, where Xaal = Leu, Ile, Met, Thr or Val; Caa2 = Val, Ala, Cys, Ile, Leu or Thr; Xaa3 = Ser, Thr or Leu; Xaa4 = Val Cor Thr; Xaa5 = Leu, Arg or Lys; Xaa6 = Leu, Met or Phe; and (i) is not cor Thr; Xaa5 = Leu, Arg or Lys; Xaa6 = Leu, Met or Phe; and (i) is not cor Thr; Xaa5 = Leu, Arg or Lys; Xaa6 = Leu, Met or Phe; and (ii) is not cor Thr; Man Pro Met Val Ala Thr Val (vi). The peptides are useful for providing immunity against future infections by HCMV, and for augmenting cor the immune reaponse of an individual who is latently infected with HCMV and is at risk for reactivation of HCMV infection. The peptides are also useful for imparting immunity to a bone marrow transplant recipient, a solid organ recipient, a heart patient, an Albs patient or a woman of confid-bearing years, without the need for ex vivo expansion of HCMV specific CTL in vitro, thus can be used in an assay to determine the capendary or an interval and those who have not been core exposed to HCMV and in the study of the Class I antigen-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic peptides useful for providing immunity against cytomegalovirus (CMV) infections, are capable of eliciting cellular
                                                                                                         Immunogenic; cytotoxic T lymphocytes; CTL; cytomegalovirus; HCMV;
infection; immune response; vaccine; immunostimulant; antiviral;
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                                                                                                                                                   immunosuppressive; immunity; immunisation.
                                                                                                                                                                                                                                                                                       /label= Leu, Phe, Met
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 29; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response to human CMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00950064.
98US-00021298.
                                                                                                                                                                                                                                                                                                                                                                                                        98US-00075257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-430383/37.
                                                                                                                                                                                          Human herpesvirus 5.
                                                                                                                                                                                                                                                                     Misc-difference 10
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                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2000
                                                                                                                                                                                                                Synthetic.
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Sequence 631 AA;

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stimulate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in vivo or in vitro immuno-stimulation of mammalian, more preferably human T lymphocytes, where the stimulated T lymphocytes are expanded and can be transfused into a patient. AAB86544-AAB86803 represent fragments of the human cytomegalovirus IEI and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
         88888888888%8
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Sequence 561 AA;

. 0 100.0%; Score 53; DB 4; Length 561; 100.0%; Pred. No. 0.87; ive 0; Mismatches 0; Indels 10; Conservative 1 TPRVTGGGAM 10 Local Similarity Query Match Matchee õ

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Gaps

417 TPRVTGGGAM 426

AAW23036 standard; protein; 631 AA. AAW23036; RESULT 15 AAW23036

Human cytomegalovirus combined antigen. (first entry) 23-MAR-1998

Human, cytomegalovirus, combined antigen, detection, antibody, vaccine, immunoglobulin A, IgA.

Human cytomegalovirus. Synthetic.

WO9731117-A2

28-AUG-1997

97WO-EP000865. 20-FEB-1997; 96US-00605541. 22-FEB-1996;

(UYMA-) UNIV MAASTRICHT.

Stals F, Bruggeman CA, Vink C,

Ramon A;

WPI; 1997-435169/40. N-PSDB; AAT79194. Combined antigen containing parts of 3 human cytomegalovirus proteins useful for early detection of virus specific antibodies and in preventative vaccines.

Example 4; Page 21; 26pp; English.

The present sequence represents a human cytomegalovirus combined antigen, which contains amino acid sequences from at least 3 human cytomegalovirus (hcWv) proteins and has an increased ability to bind hcWv specific antibodies (Ab). The device is used to detect and quantify Ab, particularly of immunoglobulin A (IgA) type, in human body fluids and tissues. The antigen is also used in vaccines for protection against diseases caused by hcWv and to generate Ab for hcWv detection. The combined antigen can detect hcWv infection at an early stage (allowing early treatment), since sensitivity and accuracy are improved by the interaction of immunodominant regions of early formed proteins present in a single antigen (the combine antigen's Ab binding ability is 2-3 times greater than for single antigens). The combined antigen also avoids the lack of antigen standardisation which limits use of conventional assay systems

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0; Gaps

90.6%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.091; ive 0; Mismatches 0; Indels

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

Sequence 10 AA;

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1 TPRVTGGGA

immunodeficient subjects. These immunological peptides can also be formulated as vaccines which are claimed to be useful for protecting against HGMV infection, augmenting the immune system response to a HCMV infection or protecting against reactivation of a latent HCMV infection

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                                                                                                                                                                                                                                                                         Immunogenic epitope; human cytomegalovirus; HCMV; vaccine; generic; CD8+; cytotoxic T-lymphocyte; MHC; major histocompatibility complex; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present generic peptide sequence is based on the sequence given in AAW48985. Sequence variants of the present peptide are recognised by the CDB+ class I major histocompatibility complex (MHC) restricted cytotoxic T-lymphocytes of patients harboring latent HCWV infection. The peptides are claimed to be capable of activating cytotoxic T-cell lymphocytes in the absence of active viral replication, and thus are useful for eliciting a cellular immune response against HCMV by normal and
                                                                                                                                                                                                                                             Generic immuno-reactive peptide CTL epitope 4 of human cytomegalovirus.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoreactive human cytomegalovirus epitopes - useful to vaccinate
                                    ;
0
        100.0%; Score 53; DB 2; Length 631; 100.0%; Pred. No. 0.98; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                AAW48986 standard; peptide; 10 AA.
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Query Match
Best Local Similarity 100.0
...rhes 10; Conservative
                                                                                           163 TPRVTGGGAM 172
                                                                1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           York J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-297862/26.
                                                                                                                                                                                                                                                                                                                                   Human herpesvirus 5.
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diamond DJ,
                                                                                                                                                                                                                                                                                                                    Synthetic.
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Sun Mar

WPI; 1997-535849/49. N-PSDB; AAT91282 27-SEP-2001 AAE10840 ð g

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This sequence comprises the full-length human cytomegalovirus (HCMV) Towne strain tegument phosphoprotein pp55; the strain AD169 pp65 sequence is given in AAW26732. The invention provides DNA molecules (see AAF12180-813 and AAT99436) useful for in vitro and in vivo expression of antigenic fragments of the HCMV genome. Preferred antigens include full-length and transmembrane-deleted fragments of gB (see AAW27274) such as gB1-6B0, phosphoprotein pp65 (see AAW27276) phosphoprotein pp65 (see AAW27277) and the Ir-exon 4 product (see AAW27275). The DNA molecule is preferably in the form of a plasmid and includes a regulatory sequence for expressing the antigen in mammals, where the antigen elicits an immune response. The products can induce HCMV-specific immune responses including neutralising antibodies and cytotoxic I lymphocytes and can be used for the prevention and treatment of HCMV infections
New human cytomegalovirus DNA constructs - encode a HCMV antigen to induce an immune response, used for the treatment and prevention of HCMV infection.
                                                                                                                                                                                                                                                   Example 3; Fig 5; 66pp; English.
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Sequence 551 AA;

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Gaps
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100.0%; Score 53; DB 2; Length 551; 100.0%; Pred. No. 0.85; tive 0; Mismatches 0; Indels
                      Best Local Similarity 100.
Matches 10; Conservative
    Query Match
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AAE10840 standard; protein; 560 AA. 18-DEC-2001 AAE10840;

Cytomegalovirus antigen pp65 protein. (first entry)

Cytomegalovirus; CMV; pp65 antigen; cytostatic; virucide; cell therapy; vaccine; viral infection; immunotherapy; gene therapy; cancer.

Cytomegalovirus

WO200170766-A2

19-MAR-2001; 2001WO-US008916.

21-MAR-2000; 2000US-0191050P. 12-DEC-2000; 2000US-0254989P.

GENZ) GENZYME CORP

Nicolette CA;

WPI; 2001-596936/67. N-PSDB; AAD18185.

vaccines and to expand immune effector cells which are specific for viral infections characterized by expression of cytomegalovirus antigen pp65. Novel synthetic antigenic compounds useful as components of antiviral

This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino acid sequence of the antigen into protein fragments (II) of at least 9 amino acids, whereby adjacent or neighbouring fragments are in the whole antigen sequence, (ii) synthesizing a peptide library containing (II); and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension comprising (II) in a single culture vessel. The method is used to immuno-

Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and

WPI; 2001-557718/62.

the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.

Example; Page 28-29; 85pp; German.

Claim 7; Page 63-64; 66pp; English.

The invention relates to synthetic antigenic compounds which are useful

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cytomegalovirus antigen constructerised by expression of COMP.

Cytomegalovirus antigen pp65. Antigenic compounds are useful for immunotherapy and also for inducing an immune response in a subject. The antigenic compound is useful for addilating immune response to the cartigenic compound is useful for addilating immune response to the cognate native ligands and their corresponding native proteins, and is useful as compounds and their corresponding native proteins, and is capanding immune effector cells that are specific for viral infections characterised by expression of CMV antigen pp65. Furthermore, the cartigenic compound also has diagnostic applications. The DNA encoding the antigenic compounds are useful as probes and primers for detecting genes antigenic compounds are useful as probes and primers for detecting genes or gene transcripts that are expressed in antigen presenting cells (APC), to confirm transduction of the polynuclectides into host cells and also in gene therapy techniques for treating cancer. The antigenic compounds immune receptor cell is also useful as vaccines. The antigenic compounds condition their DNAs are useful for preparing medicaments for diseases such as cancer. The present sequence is native CMV antigen pp65 protein
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components of antiviral vaccines and to expand immune effector cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen-specific stimulation, T-lymphocyte, CD8 stimulation, pp65; CD4 stimulation; immuno-stimulation, IB1; lower matrix phosphoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus strain AD169 pp65 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB86545 standard; protein; 561 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 TPRVTGGGAM 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                            Sequence 560 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB86545;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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   8X888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytotoxic T-lymphocyte (CTL) epitope(8) of the same or different antigen of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US1 or UL18. The peptide comprises a sequence of about 9-20 contiguous amino acids of the antigen. The peptide epitopes are useful in diagnosing, preventing or treating cytomegalovirus infection in humans, and in monitoring immune presponses in various clinical settings (e.g. transplantation or prepanancy). This sequence represents a human cytomegalovirus CTL epitope peptide of the invention
                           Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp180; gB; gH; IE-1; IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy; transplantation.
                                                                                                                                                                                                                                                                                                                                                                              New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp71, pp150, gB, gH, IR-1, IE-2, US2, US3, US6, US11 or UL18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated peptide comprising one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCMV; CMV; antigen; infection; therapy; vaccine; tegument protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 53; DB 6; Length 20; 100.0%; Pred. No. 0.026; Live 0; Mismatches 0; Indels
Human cytomegalovirus CTL epitope peptide SEQ ID No 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytomegalovirus tegument protein pp65.
                                                                                                                                                                                                                                                                                (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "encoded by AAT"
                                                                                                                                                                                                                                                                                                                   Walker SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW26732 standard; protein; 551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytomegalovirus AD169 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 106; 308pp; English.
                                                                                                                                                                                                                   26-JUN-2002; 2002WO-AU000829.
                                                                                                                                                                                                                                                  26-JUN-2001; 2001AU-00005931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                   Khanna R, Elkington RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TPRVTGGGAM 16
                                                                                                                  Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprotein pp65
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-300379/29.
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                                                                                                                                                 WO2003000720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9740165-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1998
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                                                                                                                                                                                  03-JAN-2003
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AD169 strain tegument phosphoprotein pp55; the strain Towne pp65 sequence is given in AAW27276. The invention provides DNA molecules (see AAF91280-83 and AAF99436) useful for in vitro and in vivo expression of antigenic tragments of the HCMV genome. Preferred antigens include full-length and transmembrane-deleted fragments of g8 (see AAW27274) such as g81-680, phosphoprotein pp65 (see AAW27276 and AAW27275). The Dp50 (see AAW27277) and the IE-exon 4 product (see AAW27275). The DNA molecule is preferrably in the form of a plasmid and includes a regulatory sequence for expressing the antigen in mammals, where the antigen elicits an immune response. The products can induce HCMV-specific immune responses including neutralising antibodies and cytocoxic Tlymphocytes and can be used for the prevention and treatment of HCMV infections
                                                                                                                                                                             New human cytomegalovirus DNA constructs - encode a HCMV antigen to induce an immune response, used for the treatment and prevention of HCMV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         This sequence comprises the full-length human cytomegalovirus (HCMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCMV; CMV; antigen; infection; therapy; vaccine; tegument protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                       (WIST-) WISTAR INST ANATOMY & BIOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus Towne strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW27276 standard; protein; 551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΰ
                                                                                                     Kari C;
                                                                                                                                                                                                                                             Example 3; Fig 5; 66pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0015717P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US006866
            97WO-US006866
                                          96US-0015717P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berencsi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 TPRVTGGGAM 416
                                                                                                     Berencsi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprotein pp65.
                                                                                                                                   WPI; 1997-535849/49.
N-PSDB; AAT99436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 551 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1996;
            22-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9740165-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1998
                                                                                                     Gonczol E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gonczol E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW27276;
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AAB86672 standard; peptide; 15 AA.

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Gaps

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This sequence represents a novel method for stimulating CDB or CD4 T cells for the immuno-stimulation of mammals and the determination of the cells for the immuno-stimulation of mammals and the determination of the cais sequence of the antigen into protein fragments (II) of at least 9 amino acids, whereby adjacent or neighbouring fragments are in the whole amino acids, whereby adjacent or neighbouring fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); and single culture vessel. The method is used to immunocytising (II) in a single culture vessel. The method is used to immunocytismulate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in vivo determine strength of that response. The method is suitable for in vivo or in vitro immuno-stimulation of mammalian, more preferably human T cells in the stimulation of mammalian, more preferably human T cells in the stimulation of mammalian of the stimulation of mammalian of the transfused into a patient. Alabes644—Alaba86903 represent fragments of the human cytomegalovirus IEI and pp65 lower matrix phosphoprotein which are the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65;
CD4 stimulation; immuno-stimulation; IB1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus strain AD169 pp65 peptide fragment SEQ ID 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khatamzae
                                           ;
100.0%; Score 53; DB 2; Length 15; 100.0%; Pred. No. 0.019; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surel I,
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reinke P, Faulhaber N,
                                                                                                                                                                                                                                           AAB86673 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 2; 85pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2000; 2000DE-01009341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-FEB-2001; 2001WO-EP001773
                                                                                                                                                                                                                                                                                                                                    (first entry)
                           Best Local Similarity 100.
Matches 10; Conservative
                                                                                          1 TPRVTGGGAM 10
                                                                                                                                   3 TPRVTGGGAM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-557718/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kern F, Volk H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                    20-NOV-2001
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                                                                                                                                                                                                                                                                                           AAB86673;
           Query Match
                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                            AAB86673
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This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino caid sequence of the antigen into protein fragments (II) of at least 9 caid sequence of the antigen into protein fragments are in the whole antigen sequence, (ii) synthesizing a peptide library containing (II); comprising (II) in a single culture vessel. The method is used to immunocomprising (II) in a single culture vessel. The method is used to immunocomprising (II) in a single culture vessel. The method is used to immunocomply immunologically particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has considered into immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulated T lymphocytes are expanded and can be transfused into a patient. AAB86544.AAB86803 represent fragments of the human cytomegalovirus IEI and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
                                                                                                                         Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65; CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                   Human cytomegalovirus strain AD169 pp65 peptide fragment SEQ ID 129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Khatamzas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 53; DB 4; Length 15; 100.0%; Pred. No. 0.019;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Volk H, Reinke P, Faulhaber N, Surel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ38030 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 2; 85pp; German.
                                                                                                                                                                                                                                                                                                      17-FEB-2001; 2001WO-EP001773
                                                                                                                                                                                                                                                                                                                                        22-FEB-2000; 2000DE-01009341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                        Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-557718/62.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                               (KERN/) KERN F.
                                                                                                                                                                                                                              WO200163286-A2
                                                       20-NOV-2001
                                                                                                                                                                                                                                                                    30-AUG-2001
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                   AAB86672;
                                                                                                                                                                                                                                                                                                                                                                                                                       Kern F,
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0; Gaps

100.0%; Score 53; DB 4; Length 15; 100.0%; Pred. No. 0.019; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 10; Conservative

Query Match

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related Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and haematopoietic malignant tumours such as leukaemia and lymphoma. The aptitope is an HIA, (human leukocyte antigen) peptide derived from a viral orlumour antigen. The present sequence is a viral HIA epitope used in the fusion proteins of the invention

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New polynucleotide capable of expressing an epitope-beta2m fusion protein useful for generating cytotoxic I lymphocyte responses against a tumor and in restoring antigen presentation in the tumor of a host.
sequence is an HCMV pp65 protein immunogenic epitope upon which vaccines and peptides of the invention are based
                                                                                                                                                                                                                                                                                                                                                                                                                                   prostatic cancer; testicular cancer; lung cancer; breast cancer; malignant melanoma; mesothelioma; brain tumour; ovarian cancer; uterine cancer; cervical cancer; head and neck cancer; bladder cancer; Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma; acquired immunodeficiency syndrome; AIDS-related lymphoma.
                                                                                                                                                                                                                                                                                                                                                                        Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA; human leukocyte antigen; fusion protein; epitope; cytostatic; tumour; gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer; liver cancer; biliary trac cancer; pancreatic cancer; vaccine;
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G, Hunter M;
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                           Cytomegalovirus lower matrix protein pp65 HLA-B0702 epitope.
                                                                              100.0%; Score 53; DB 5; Length 10; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      ABG66768 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001; 2001WO-GB004844.
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                              10; Conservative
                                                                                                                                            1 TPRVTGGGAM 10
                                                                                                                                                                           1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus.
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                                                                                              Best Local Similarity
                                                   Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2002.
                                                                                                                                                                                                                                                                                                                24-SEP-2002
                                                                                   Query Match
                                                                                                                 Matches
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ABG66768
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The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintaining immunologic CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a monogene antigen, a multilineage antigen, an embryonic antigen, an oncogene antigen, a multated tumour-suppressor gene antigen, or a viral antigen. They can be used for the treatment of antigen, or a viral antigen. They can be used for the treatment of antigen, or a viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes blace in the milieu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAY10071 to AAX10639 represent examples of peptide antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
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                                                                                                                                      100.0%; Score 53; DB 5; Length 10; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                         AAY10218 standard; peptide; 15 AA.
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Matches 10; Conservative
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Sequence 15 AA;

The invention relates to a new polynuclectide capable of expressing an epitope-beta 2m fusion protein useful for generating cytotoxic T

Tymphocyte (CTL) responses against a tumour or in restoring antigen to presentation in the tumour of a host. Also included are a polynuclectide capable of expressing an epitope-beta 2m fusion protein in combination with a vaccination agent that stimulates a CTL response against the epitope of the fusion protein for simulates a CTL response against the use in the treatment of cancer and a method of treating a tumour by administering a capable of expressing an epitope-beta 2m fusion protein, and optionally a vaccination agent that stimulates a CTL response against the epitope of the fusion protein. The polynucleotide is useful for the epitope of the fusion protein. The polynucleotide is useful for generating CTL responses against tumours, for restoring antigen protein in the tumour, and subsequently for treating cancers, such as gastrointesfriant unmour, protatic, testicular, lung or breast cancer, malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine cancer including cervical cancer, cancer of the head and neck, bladder cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome)-

Disclosure; Page 24; 46pp; English.

New peptides that are immunogenic epitopes of the human cytomegalovirus (CMV), useful for activating cytotoxic T lymphocytes (CTL) or CTL precursors to elicit an immune response against human CMV by normal or WPI; 2001-431950/46. Diamond DJ, AAE05431; (YORK/) Matches 8888888888888888 δ

ö useful for imparting immunity to a bone marrow transplant recipient, a solid organ recipient, a heart patient, an AIDS patient or a woman of child-bearing years, without the need for ex vivo expansion of HCWV-specific CTL. These peptides can directly stimulate cytotoxic T lymphocytes (CTL) in vitro, thus can be used in an assay to determine the degree of immunostimulation caused by HCMV. These may also be used to distinguish individuals who are seropositive from those who have not been exposed to HCMV and in the study of the Class I antigen-processing pathway for HCMV proteins. The present sequence represents a peptide used in the exemplification of the present invention and is at risk for reactivation of HCMV infection. The peptides are also useful for imparting immunity to a hone marrow transfort to a hone marrow transfort. 0; Gaps Human cytomegalovirus; HCMV; cytotoxic epitope; infection; vaccine; cytotoxic T lymphocyte; CTL; CTL precursor; CTLp; Class I antigen; major histocompatibility complex; MHC; cellular immune response; CTL activator; CTLp activator; immunostimulant. Human cytomegalovirus (HCMV) minimal cytotoxic epitope #3. 100.0%; Score 53; DB 3; Length 10; 100.0%; Pred. No. 0.012; 0; Indels 0; Mismatches AAE05431 standard; peptide; 10 AA. 96US-00747488. 97US-00950064. 98US-00021298. 27-MAR-2000; 2000US-00534639. 98US-00075257 (first entry) 10; Conservative 1 TPRVTGGGAM 10 1 TPRVTGGGAM 10 Human cytomegalovirus. DIAM/) DIAMOND D J. Query Match Best Local Similarity YORK J. Sequence 10 AA; US6251399-B1. 11-MAY-1998; 12-NOV-1996; 10-FEB-1998; 24-SEP-2001 26-JUN-2001

The invention relates to immunogenic peptides derived from human cytomegalovirus (HCMV) which are recognised by human cytotoxic T[Style of the invention also discloses a vaccine against HCMV comprising one of the peptides, and a pharmaceutically acceptable comprising one of the peptides, and a pharmaceutically acceptable carrier, a cellular vaccine against HCMV comprising antigen presenting carrier. The vaccine is used to modulate the immune response to human expension of the vaccine is used to modulate the immune response to human cytomegalovirus infection. HCMV is implicated in a number of diseases and conditions including restencish after coronary angioplasty.

Conditions including restencial after coronary angioplasty.

Conditions including restencial after to blindness, encephalitis, enteritis, patients, viral retinitis leading to blindness, encephalitis, enteritis, companically interstitial pneumonia, malignancy (e.g. Karposi's sarcoma) and post-bone marrow transplant complications. The present ó for activating CTLs and CTL precursors (CTLp), particularly for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The peptides may be used in an assay for determining the degree of immunostimulation caused by HCMV. The peptides may also be used for distinguishing individuals who are scropositive from those who have not seen exposed to HCMV (seronegative individuals). The present peptide sequence is a minimal cytotoxic epitope from human cytomegalovirus. This sequence has allele specificity to HLA B7 and subtypes New immunogenic peptides useful as a vaccination against cytomegalovirus infection, comprises epitopes of human cytomegalovirus which are recognized by human cytotoxic T-lymphocytes. Immunogenic epitope; pp65; cytotoxic T cell; CTL; HCMV; vaccine; virucide; restenosis; coronary angioplasty; morbidity; mortality; AIDS; acquired immunodeficiency syndrome; viral retinitis; blindness; encephalitis; enteritis; mononucleosis; interstitial pneumonia; malignancy; Karposi's sarcoma; post-bone marrow transplant complication. Gaps ; 0 100.0%; Score 53; DB 4; Length 10; 100.0%; Pred. No. 0.012; Human cytomegalovirus pp65 protein immunogenic epitope #4. 0; Indels 0; Mismatches AAU10826 standard; peptide; 10 AA. Claim 12; Page 28; 65pp; English 27-MAR-2000; 2000US-00534639. 20-OCT-2000; 2000US-00692170. 16-MAR-2001; 2001WO-US008576. (first entry) Local Similarity 100. es 10; Conservative 1 TPRVTGGGAM 10 1 TPRVTGGGAM 10 Human cytomegalovirus. (CITY) CITY OF HOPE. WPI; 2002-041233/05. WO200172782-A2. Sequence 10 AA; 14-FEB-2002 04-OCT-2001 Diamond DJ; AAU10826; Query Match Matches RESULT 5 AAU10826 8\$8888888\$\$ à

The invention relates to immunologically active peptides, and functional variants thereof, capable of eliciting a cellular immune response to thuman cytomegalovirus (RFMV) in humans. The peptides are capable of directing human cytocoxic T lymphocytes (CTL) to recognise and lyse human cells infected with HCMV. Such immunologically active peptides, in association with an major histocompatibility complex (MHC) class I molecule, are recognised by CTEs of individuals having a latent (inactive) HCMV infection. Vaccines comprising these peptides are useful

Example 14; Col 7; 17pp; English.

immunodeficient subjects.

York J;

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Immunoreactive human cytomegalovirus epitopes - useful to vaccinate
                                             against infection.
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Claim 9; Page 49; 56pp; English.

The present peptide is an immunogenic epitope which is recognised by the CD8+ class I major histocompatibility complex (MHC) restricted cytotoxic T-lymphocytes of patients harboring latent HCMV infection. The peptide is claimed to be capable of activating cytotoxic T-cell lymphocytes in the absence of active viral replication, and thus is useful for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The immunological peptide can also be formulated as a vaccine which is claimed to be useful for protecting against HCMV infection, augmenting the immune system response to a HCMV infection, against reactivation of a latent HCMV infection

Sequence 10 AA;

0; Gaps 100.0%; Score 53; DB 2; Length 10; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 10; Conservative Query Match

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RESULT 2 AAY09322

AAY09322 standard; peptide; 10 AA.

AAY09322;

(first entry)

08-JUL-1999

Immunogenic peptide cytotoxic T lymphocyte epitope SEQ ID NO:7 of hCMV.

immune response; cytotoxic T lymphocyte; CTL; immunostimulation; infection; immunosuppression; bone marrow transplant; solid organ; heart; Human cytomegalovirus; hCMV; immunologically active peptide; vaccine;

Human herpesvirus 5. Synthetic.

W09919349-A1

22-APR-1999

98WO-US009652. 11-MAY-1998; 97US-00950064. 98US-00021298 10-FEB-1998; 14-0CT-1997;

(CITY) CITY OF HOPE.

York J;

Diamond DJ,

WPI; 1999-277590/23

Immunogenic peptide cytotoxic T lymphocyte epitopes of human cytomegalovirus.

Claim 9; Page 50; 64pp; English.

capable of eliciting a cellular immune response to human cytomegalovirus (hCMV). The IAP can be used in a (cellular) vaccine to augment the immune system response to HCMV, or to provide immunity against HCMV. The IAP cellular) vaccine can also protect an individual having a latent HCMV infection from reactivation. An antigen presenting cell can be used to determine the presence or absence of HCMV-infected T lymphocytes. The viral vector containing IAP encoding DNA can also be used to provide present invention describes immunologically active peptides (IAPs)

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                                                                             HCMV can cause opportunistic infections resulting in a variety of complications in, e.g. immunosuppressed patients. The IAP vaccines impart immunity to bone marrow transplant recipients, solid organ recipients, heart patients, AIDS patients or women of child-bearing years, without the need for ex vivo expansion of HCMV-specific cytotoxic T lymphocytes (which requires sophisticated laboratory setup and is highly labor-
immunity against HCMV. The IAP can be used to prepare HCMV-reactive human
               cytotoxic T lymphocytes. The antigen presenting cells primed with the IAPs can be used as diagnostic reagents to detect immunostimulation by HCMV. They can also detect active HCMV infection or exposure to HCMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic peptides useful for providing immunity against cytomegalovirus (CMV) infections, are capable of eliciting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic; cytotoxic T lymphocytes; CTL; cytomegalovirus; HCMV; infection; immune response; vaccine; immunostimulant; antiviral; immunosuppressive; immunity; immunisation.
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98US-00021298.
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US-10-697-055-7 53 Title: Perfect score:

1 TPRVTGGGAM 10 Scoring table: Sequence:

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1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

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Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 66552, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

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APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Pants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 66952

LENGRIH: 383

TUDE: NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09895593

Sequence 2, Application US/09895593

Patent No. US2020160949A1

GENERAL INFORMATION:

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APPLICANT: Leonard, Warren J.

APPLICANT: Leonard, Warren J.

APPLICANT: Lodish, Harvey F.

ITILE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and

ITILE OF INVENTION: Uses Thereof

FILE REFERENCE: 00-514-E

CURRENT APPLICATION NUMBER: US/09/895,593

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 2

LENGTH: 370

TURE OF THE PATENTION: USES THE PRIOR PRIOR
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Pred. No. 6e+02;
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                                    7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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; Sequence 3, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Baumann, Heinz
; APPLICANT: Baumann, Heinz
; APPLICANT: Farr, Andrew G.
; APPLICANT: Leonard, Warren D.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Uses Thereof
; TITLE OF INVENTION: Uses Thereof
; TITLE OF LINIOR INCOMERR: US/09/895,593
; CURRENT APPLICATION NUMBER: US/09/895,593
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i Sequence 3, Application US/09895943

j Patent No. US20020068323A1

j GENERAL INFORMATION:

APPLICANT: Garis, Chris

APPLICANT: Chang, Ming-Shi

ITILE OF INVENTION: Uses Thereof

FILE REPRESENCE: 00-514-C

CURRENT APPLICATION NUMBER: US/09/895,943

CURRENT PILING DATE: 2001-06-28

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 16

SOUTWARE: Patentin Ver. 2.0

SEQ ID NO 3

IENGTH: 353

TYPER: PATENTIAN OF THE CONTROL NUMBER: CONTROL OF CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 35; DB 9; Length 353; 77.8%; Pred. No. 5.7e+02; vative 0; Mismatches 2; Indels
                                                                                                                                                                                                            CTHER INFORMATION: Orthologous to G1652
US-10-374-780A-1701
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PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
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Best Local Similarity 77.5
Best Local Similarity 77.5
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; LOCATION: (227)..(247)
US-09-895-943-3
                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |||||
91 SPHVTGGG 98
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                                       SEQ ID NO 1701
LENGTH: 338
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APPLICANT: Chang, Ming-Shi
TTLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 00-514-C
CURRENT APPLICATION NUMBER: US/09/895,943
CURRENT PILING DATE: 2001-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
LENGTH: 370
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Pred. No. 5.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOHNEAN INCOMPAILON:
JAPPLICANT: Cabezon-Silva, Teresa Elisa Virginia
APPLICANT: Cache, Thierry
APPLICANT: Ganlis, Swann Romain Jean-Thomas
APPLICANT: Ganlis, Swann Romain Jean-Thomas
APPLICANT: Cassart, Jean-Pol
TITLE OF INVENTION: Thumour-Specific Animal Proteins
FILE REPRENCE: EC45300-1
CURRENT FILING PATE: 2002-12-05
NUMBER OF ESQ ID NOS: 33
SOFTWARE: FRASEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-895-943-2

Sequence 2, Application US/09895943

Patent No. US20020068323A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10226872; Publication No. US20030157118A1; GENERAL INFORMATION:
                                                                                                                                                                                                               66.0%;
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 353
                                                                                                                                                                                           Query Match
Best Local Similarity 77.0

Best Tocal 7; Conservative
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                                                                                                                                                                                                                                                                                                      2 PRVTGGGAM 10
                                                                   TYPE: PRT ORGANISM: Mus musculus
                                                                                                           ; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (227)...(247)
US-09-895-593-3
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; ORGANISM: Human
US-10-226-872-7
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APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaria
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REPERENCE: MBI-0047 CIP
CURRENT APPLICATION WUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 14; Length 330;
Pred. No. 5.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                  FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-02
NUMBER: OF SEQ ID NOS: 15109
LENGTH: 230
                                                                               APPLICANT: SHTBA, TADAVOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-04-18
PRIOR PELING DATE: 2001-04-18
PRIOR PELING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/136,049
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces avermitilis US-10-156-761-9249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
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Haake, Volker
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Adam, Luc J
Reuber, T. Lynne
Keddie, James
Broun, Pierre E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                    APPLICANT:
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APPLICANT
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53.23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220062
LENGTH: 231
                                                                                                                      Sequence 206428, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
APPLICANT: Covalic David K
APPLICANT: APPLICANT: Application Wilma
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE REFERENCE: 38-21 (53223) B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206428
LENGTH: 163
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Best Local Similarity 60.0%; Pred. No. 3.88+02;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.0%; Score 35; DB 12; Length 163; Best Local Similarity 85.7%; Pred. No. 2.7e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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US-10-424-599-220062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28431C.1.pep
US-10-424-599-206428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9249, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 řPŘIŤĠCĠIL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 PRVSGGG 81
          21 PRAIGGG 27
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                                                                                          RESULT 40
US-10-424-599-206428
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US-10-156-761-9249
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Gaps

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Sequence 258345, Application US/10424599
| Sequence 258345, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Alou Yihua
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION NUMBER: US/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 285684
| SEQ ID NO 258345
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                          1; Indels
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US-10-424-599-255296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_7530C.1.pep
US-10-424-599-258345
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66.0%; Score 35; DB 12;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1;
75.0%; Pred. No. 1.1e+02;
tive 1; Mismatches 1;
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.79
Matches 6; Conservative
  Best Local Similarity 75.03
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                    33 SPEVTGGG 40
                                                                           1 TPRVTGGG 8
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Sequence 207115, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwel

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 207115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10 ($2052)
FILE REFERENCE: 38-10 ($2052)
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10058
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87.5%; Pred. No. 9.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                       67.9%; Score 36; DB 12; Length 768; 75.0%; Pred. No. 8.4e+02; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: magnetite-containing magnetic coccus US-10-369-493-10058
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10058, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                          NAME/KEY: MISC_FEATURE
1 COCATION: (479)..(479)
1 OTHER INFORMATION: X=any amino acid
US-10-282-1228-45835
                 OTHER INFORMATION: X=any amino acid
                                                                                                                                                           Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5'
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                  374 PRIPGGGA 381
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US-10-424-599-207115
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US-10-369-493-10058
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RESULT 39
US-10-42-599-255296
US-10-42-599-255296
Sequence 255266, Application US/10424599
Sequence 255266, Application US/10424599
Sequence 255266, Application US/10424599
Publication No. US20040031072AI
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Town Vihua
APPLICANT: Town Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(55223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NO 255296
LENGTH: 153
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66.0%; Score 35; DB 12; Length 69;

Query Match

us-10-697-055-7.rapb

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APPLICANT: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-09
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LOCATION: (382)..(382)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (114)..(114)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (116)...(116)
OTHER INFORMATION: X=any amino acid
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LOCATION: (319)..(319)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE
LOCATION: (348)..(348)
OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
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LOCATION: (360)...(360)
OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
                            Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus anthracis
Zyskind, Judith
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewn C.
APPLICANT: Slater, Stewn C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20821
LENGTH: 600
                                                             APPLICANT: Zhou, Yihua Javid K. APPLICANT: Zhou, Yihua Javid K. APPLICANT: Kovallc, David K. APPLICANT: Kovallc, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DAIE: 2003-04-28

SEQ ID NO 70152

LENGTH: 560
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100.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: UC-ZMFLB73061A02_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Sequence 45835, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Malone, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 20821, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
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; ORGANISM: Rhodopseudomonas palustris
US-10-369-493-20821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.8
Matches 7; Conservative
                         APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 rpksrcsca 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-10-369-493-20821
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Query Match
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                                                                                                                                                                                                                                                  Sequence 15690, Application US/10369493
; Sequence 15690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: APPLICANT: Blater. Steven C.
    APPLICANT: APPLICANT: Stater Steven C.
    APPLICANT: APPLICANT: APPLICANT: Stater S.
    APPLICANT: APPLICANT: Chen, Xianfeng
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERTIES
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
    TITLE OF INVENTION NUMBER: US/10/369,493
    CURRENT FILING DATE: 2003-02-28
    PRIOR PELICATION NUMBER: US 60/360,039
    PRIOR PILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15690
; TENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16082, Application US/10369493
; Bublication No. US20030233675A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, PLANTS WITH IMPROVED PROPERTIES
    ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TURRENT APPLICATION NUMBER: US/10/369,493
    CURRENT FILING DATE: 2003-02-28
    PRIOR FILING DATE: 2002-02-21
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 16082
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67.9%; Score 36; DB 14; Length 244; 70.0%; Pred. No. 2.7e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 67.9%; Score 36; DB 15; Length 276; Best Local Similarity 66.7%; Pred. No. 3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Xanthomonas campestris US-10-369-493-15690
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Best Local Similarity 66.797
-hes 6; Conservative
                       Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                  1 TPRVTGGGAM 10
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                                                                                                                                           74 TPRPTGGAKM 83
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     Query Match
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## Sequence 15324, Application US/10369493

| Sequence 15324, Application US/10369493
| Publication No. US20030233675A1
| GENERAL INFORMATION:
| APPLICANT: Co., Yongwei
| APPLICANT: Goldman, Barry S. |
| APPLICANT: Ghoi, Xianfeng |
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES |
| TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES |
| FILE REFERENCE: 38-10 (52052) B |
| CURRENT APPLICATION NUMBER: US/10/369,493 |
| PRIOR FILING DATE: 2003-02-28 |
| PRIOR FILING DATE: 2003-02-21 |
| NUMBER OF SEQ ID NOS: 47374 |
| SEQ ID NO 15324 |
| LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven B
APPLICANT: Screen, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Done Invention: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64171
LENGTH: 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%; Score 36; DB 12; Length 346; 75.0%; Pred. No. 3.8e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: LIB3593-009-E11_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
US-10-425-114-70152
; Sequence 70152, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 64171, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0 Matches 6; Conservative
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242 TPRLTGSGS 250
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54 TPRMAGGG 61
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ORGANISM: Zea mays
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US-10-425-114-64171
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hank David R.
APPLICANT: Hank David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: BACHICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27829
LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO ALL133476.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN DLACENTA, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
                             1; Indels
  Pred. No. 60;
3; Mismatches
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WASAHIRA
ITILE OF INVENTION: NOVEL FOLYNUCLECTIDES
FILE REPREMENC: 249-262
CURRENT PILING DATE: 2002-05-29
RIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-272697
NUMBER OF SEQ ID NOS: 15109
SERVICE SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15056, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            Sequence 27829, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
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  60.0%;
                                6; Conservative
                                                                                    1 TPRVTGGGAM 10
                                                                                                                    :| :|||||:
28 SPYMTGGGAL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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US-10-029-386-27829
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Sequence 180013, Application US/10424599

Bublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cov Vinua

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFRENCE: 38-21(53.23.)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
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                                                                                                               Query Match 69.8%; Score 37; DB 14; Length 748; Best Local Similarity 75.0%; Pred. No. 5.6e+02; Matches 6; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT3847_133567C.1.pep
US-10-424-599-180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13012, Application US/10156761
FUDLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIKAWA, UUN
APPLICANT: SHIRAWA, TOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: ARAKHIKA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
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CURRENT PAPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PALICATION NUMBER: JP 2001-272697
PRIOR PLING DATE: 2001-08-02
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  ; TYPE: PRT
; .ORGANISM: Streptomyceв avermitilis
US-10-156-761-12713
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US-10-156-761-13012
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SEQ ID NO 13012
LENGTH: 54
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                                                                                                                                                                                                                                 2 PRVTGGGA 9
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Best Local Similarity
Matches 6; Conserv
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US-10-156-761-13012
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LENGTH: 39
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APPLICANT: Gajiwala, Ketan S.
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Bauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
TITLE OF INVENTION: MONOUCLEOTIDE BINDING PROTEIN (FMNBP)
FILER REFERENCE: 52498-20011.00
CURRENT APPLICATION NUMBER: US/10/306,762
CURRENT APPLICATION NUMBER: US 60/334,132
PRIOR RILING DATE: 2003-04-16
PRIOR FILING DATE: 2001-11.28
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                               69.8%; Score 37; DB 12; Length 121; 77.8%; Pred. No. 91; tive 0; Mismatches 2; Indels
                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_60138C.1.pep
US-10-424-599-241541
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Sequence 12713, Application US/10156761

Sequence 12713, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: CHEBA, HARNO

APPLICANT: ISHIKAMA, HIROSHI

APPLICANT: SHIRA, TARANOSHI

APPLICANT: SHIRA, TARANOSHI

APPLICANT: SHIRA, TARANOSHI

APPLICANT: HATYOR! WASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR PLING DATE: 2001-05-30

PRIOR PLING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 109, Application US/10306762
publication No. US20030187220A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: C. aurantiacus (22971932)
US-10-306-762-109
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SEQ ID NO 12713
LENGTH: 748
                                                                                                                                                                                                    Query Match 69.8
Best Local Similarity 77.8
Matches 7; Conservative
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98 SPKVTGGG 105
                                                                                                                                                                                                                                                                                                                                                         55 TPTFTGGGA 63
                                                                                                                                                                                                                                                                                                         1 TPRVTGGGA 9
                                                                     ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPRVTGGG 8
SEQ ID NO 241541
LENGTH: 121
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US-10-306-762-109
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                                                  TYPE: PRT
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F Sequence 241541, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Vongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Volume and Uses Thereof for Plant Improvement

FILE REFREENCE: 38-21(53223)8

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 232152
LENGTH: 70
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Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_51655C.1.pep
US-10-424-599-232152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 232152, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                             PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 2884
LENGTH: 383
                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
          FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: G2373
US-10-374-780A-2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 TPRNTGGG 27
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US-10-424-599-241541
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US-10-424-599-232152
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Sequence 70467, Application US/10425114

Sequence 70467, Application US/2040034888A1

Publication No. US/2004003488BA1

GENERAL INPORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soreen, Steven E
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Paplicant: Repert Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(53313)B
CURRENT APLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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APPLICANT: BIOMIN, MESSAR L
APPLICANT: Pinded: Omaira
APPLICANT: Pinded: Omaira
APPLICANT: Pinded: Omaira
APPLICANT: Pinded: Omaira
APPLICANT: VV. Guo-Liand
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MED: 003-02-25
FILE REFERENCE: MED: 003-02-25
PRIOR PAPLICATION NUMBER: 09/837,944
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-08-25
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-10-8-22
PRIOR PILING DATE: 2001-11-3
PRIOR PILING DATE: 2001-11-3
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER INFORMATION: Clone ID: UC-ZMFLM017259F06_FLI.pep
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Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Riechmann, Osse Luis
APPLICANT: Tiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jacqueline E
APPLICANT: Haard, Jacqueline E
APPLICANT: Haard, Jacqueline E
APPLICANT: ARACHIEFE, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
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Keddie, James
Broun, Pierre E
                     7 TPRTIGGGA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
US-10-374-780A-2854
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APPLICANT:
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APPLICANT: Kovalic David K
APPLICANT: An Our Yibua
APPLICANT: Zhou Yibua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: 18/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                                     GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Grasemian, Majid
APPLICANT: Cooper, Steven P.
APPLICANT: Goff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Race, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Provart, Nicholas
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Noughers: 1009-04
FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US 60/370,743
FRIOR FILING DATE: 2003-04-04
FRIOR APPLICATION NUMBER: US 60/370,620
FRIOR APPLICATION NUMBER: US 60/370,620
FRIOR APPLICATION NUMBER: US 60/370,620
FRIOR FILING DATE: 2002-04-04
FRIOR APPLICATION NUMBER: US 60/370,620
FRIOR PLING DATE: 2002-04-04
FRIOR DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.6%; Score 39; DB 15; Length 665; 60.0%; Pred. No. 2.3e+02; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_8558C.1.pep
US-10-424-599-269734
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OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
Publication No. US20040010815A1 GENERAL INFORMATION:
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Best Local Similarity 77.00
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Best Local Similarity 60.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Oryza sativa
US-10-259-194A-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unBure
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US-10-424-599-269734
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1 TPRVTGGGA 9

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Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
                                       Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
Pena, Carol EA
                                                                                                                                                       Tcherney, Velizar T
Zerhusen, Bryan D
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
                                                                                                                                                                                                                                                           Smithson, Glennda
Baumgartner, Jason
                      Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                   Herrman, John L
Peyman, John A
Gorman, Linda
Mezes, Peter D
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Ellerman, Karen
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Best Local Similarity 75.0
Matches 6; Conservative
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43 PRITGGGS 50
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                                                            APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT APPLICATION NUMBER: 00/268,595
PRIOR PELING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
NUMBER OF SEQ ID NOS: 269
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US-10-051-874-87
; Sequence 87, Application US/10051874
; Publication No. US20040005557A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
**POTICANT: Boldog, Ferenc
                                                          Smithson, Glennda
Baumgartner, Jason C
Herrman, John L
Peyman, John A
Gorman, Linda
                                                                                                                                                                                Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
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Ellerman, Karen
Rothenberg, Mark
Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Rattus norvegicus US-10-051-874-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:||||:
43 PRITGGGS 50
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
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| APPLICANT: Richeman, Asten
| APPLICANT: Rotherhaely Mark APPLICANT: Stochenberg Mark SAME SAME
| TITLE OF INVENTION: PROTEINS, POLYNUCLECTIDES ENCODING THEM AND METHODS OF TITLE OF INVENTION: PROTEINS APPLICANTON NUMBER: UG/10/51,874
| CURRENT APPLICANTON NUMBER: UG/10/52,585
| PRIOR APPLICANTON NUMBER: GO/26,587
| PRIOR PELING DATE: 2001-09-25 |
| PRIOR PELING DATE: 2001-09-25 |
| PRIOR PELING DATE: 2001-09-25 |
| PRIOR PELING DATE: 2001-09-26 |
| PRIOR PELING DATE: 2001-09-27 |
| PRIOR PELING DATE: 2001-09-26 |
| PRIOR PELING DATE: 2001-03-6 |
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Taylor, Sarah
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TYPE: PRT
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APPLICANT:
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                                                                                                                                                                                                              APPLICANT Taylor, Valiar T
APPLICANT Taylor, Valiar T
APPLICANT Tehernev, Veliar T
APPLICANT Gloog, Ference L
APPLICANT Gloog, Ference L
APPLICANT Gloog, Ference L
APPLICANT Alsobrock II, John P
APPLICANT Garlach, Valerie L
APPLICANT Rainen, Waren
APPLICANT Rainen, Karen
APPLICANT Rainen, Karen
APPLICANT Rainen, Karen
APPLICANT Rochenberg, Mark E
APPLICANT Rochenberg, Mark E
APPLICANT Rochenberg, Mark E
APPLICANT Smithson, Glennda
APPLICANT Score, David
ITLE OF INVENTION Proteins, Polynuclectides Encoding Them and Methods of
ITLE OF INVENTION Proteins, Polynuclectides Encoding Them and PRICATION NUMBER: 60/260,417
FILE REFERENCE: 2100-257
CURRENT FILING DATE: 2001-01-09
FRIOR FILING DATE: 2001-02-28
FRIOR FILING DATE: 2001-02-28
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR PILING DATE: 2001-03-09
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73.6%; Score 39; DB 12; Length 342;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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US-10-042-865-154
; Sequence 154, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
    APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Casman, Bryan D
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shong, Mei
; APPLICANT: Though Mei
; APPLICANT: Burgess, Catherine E
, DDT.ICANT: Burgess, Catherine E
, DDT.ICANT: Burgess, Catherine E
                                                        Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
                                                                                                                                            Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Vernet, Corine A.M
Shenoy, Suresh G
Spytek, Kimberly
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; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-042-865-152
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43 PRITGGGS 50
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APPLICANT: Tilentary, Valiant T
APPLICANT: Tilentary, Valiant T
APPLICANT: Col. Miller: Charles E
APPLICANT: Charles E
APPLICANT
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Sequence 151, Applica
Publication No. US200
GENERAL INFORMATION:
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APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Secondary Glennda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
ITILE OF INVENTION: Using the Same
FILE REFERENCE: 2142-537
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 153
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
TITLE OF INVENTION: ACTIVATING PROTEASE I (CAPI) GENE DISRUPTIONS
FILE REFERENCE: R-490
CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT APPLICATION NUMBER: US 60/280,509
FRIOR FILING DATE: 2001-03-29
FRIOR FILING DATE: 2001-03-29
FRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELS 2001-08-08
SOFTWARE: FASELSEQ for Windows Version 4.0
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.6%; Score 39; DB 12; Length 339; Best Local Similarity 75.0%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 0; Indels
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US-10-109-616-2
; Sequence 2, Application US/10109616
; Sellication No. US20030167484A1
; GENERAL INFORMATION:
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CORGANISM: Mus musculus
US-10-042-865-153
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Matches 6; Conserv
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RESULT 12 US-10-042-865-151

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APPLICANT: Mallet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Seyman, John
APPLICANT: Seyman, John
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
TITLE OF INVENTION: Protections, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT PELLING DATE: 2002-05-17
FRIOR APPLICATION NUMBER: 60/260,417
FRIOR APPLICATION NUMBER: 60/260,831
FRIOR FILING DATE: 2001-01-09
FRIOR PELLING DATE: 2001-03-09
FRIOR APPLICATION NUMBER: 60/274,876
FRIOR APPLICATION NUMBER: 60/274,876
FRIOR APPLICATION NUMBER: 60/284,704
FRIOR APPLICATION 
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Application US/10042865
5. US20040029216A1
                                                                                                                                                                                                                                                                                                                           Dibong, Mei
Cangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
Tchernev, Velizar
Miller, Charles E
Guo, Xiaojia
Boldog, Ference L
Grosse, William M
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Gerlach, Valerie in
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
                                                                                                             APPLICANT: Padigaru, Muralidhara
                                                                                                                                                               Li, Li
Zerhusen, Bryan D
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ORGANISM: Rattus norvegicus
US-10-042-865-151
                                                                                                                                                                                                                              Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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Best Local Similarity
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us-10-697-055-7.rapb

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APPLICANT: Rethenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: BOOTEIN, POLINUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
TILLE OF INVENTION NUMBER: US/10/051,874
CURRENT APPLICATION NUMBER: 06/265,55
FRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-09-27
PRIOR PELING DATE: 2001-09-27
PRIOR PELING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/265,587
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-31
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Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
Tchernev, Velizar T
Miller, Charles E
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Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
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Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0%
                  Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Variant human cytomegalovirus peptide epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.6%; Score 48; DB 14; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 0.1
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = L, F or M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/10051874 Publication No. US20040005557A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baumgarther, Jason C
Herrman, John L
Peyman, John A
Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caupier Jr, Raymond J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
APPLICANT: Vernet, Corine AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Shimkete, Richard A
Pena, Carol EA
Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li, Li
Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerlach, Valerie
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Millet, Isabelle
Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lepley, Denise M
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-405-231-8
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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Gaps

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APPLICANT: Diamond, Don J. TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS FILE REFERENCE: 1954-346 CURRENT APPLICATION NUMBER: US/10/405,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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TITLE OF INVENTION:

FILE REFERENCE: 1954-398

CURRENT APPLICATION HCMV- REACTIVE T CELLS AND USES THEREFOR

FILE REFERENCE: 1954-398

CURRENT APPLICATION NUMBER: US 09/692,170

PRIOR PHILOGATION NUMBER: US 09/692,170

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-01-10

PRIOR PLILING DATE: 1998-01-10

PRIOR PLILING DATE: 1998-01-10

PRIOR FILING DATE: 1998-01-10

PRIOR FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATECHIN VERSION 3.1
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 14; Length 10;
Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.6%; Score 48; DB Best Local Similarity 100.0%; Pred. No. 0.1. Matches 9; Conservative 0; Mismatches
                                                                                                                    TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-223-538-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE

DCATION: (10)..(10)

OTHER INFORMATION: Xaa = L, F or M

US-10-238-607-8
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; Sequence 8, Application US/10405231
; Publication No. US20030190328A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/10238607; Publication No. US20030118602A1; GENERAL INFORMATION:
                                                                            LENGTH: 579 amino acids
TYPE: amino acid
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                             407 TPRVTGGGAM 416
                                                                                                                                                                                                                                                                                                                                                           1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPRVTGGGA 9
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Kari, Ceaba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 53; DB 14; Length 579; Best Local Similarity 100.0%; Pred. No. 0.9; Matches 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Wistar Institute of, Anatomy & Biology
Gonczol, Eva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-Aug-2002
CLASSIFICATION AUMBER: US/09/171,699
RILING DATE: 19-Tan-1999
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOGICEÉ, CACHY A.
REGISTRATION NUMBER: 33,980
REGISTRATION NUMBER: 33,980
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-Aug-2002
CLASSIFICATION: CURANOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
FILING DATE: 19-Gan-1999
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1966
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REGISTRATION INTHER: WST66APCT
TELECOMMINICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 215-540-8018
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10223538; Publication No. US20030120060A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 TPRVTGGGAM 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-223-538-6
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100.0%; Score 53; DB 9; Length 561; 100.0%; Pred. No. 0.87; tive 0; Mismatches 0; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 561 TYPE: PRT
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ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10434982; Publication No. US20030199673A1; GENERAL INFORMATION:
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STATE: Pennsylvania
COUNTRY: USA
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                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                ORGANISM: Homo sapiens
                                                                                                                            ; OKGA12-079A-2
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Sequence 7, Application US/10465231

Publication No. US20030190328A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: INMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS

FILE REFERENCE: 1954-346

CURRENT PILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US/09/692,170C

PRIOR APPLICATION NUMBER: US/09/692,170C

PRIOR APPLICATION NUMBER: US 09/534,639

PRIOR PILING DATE: 2000-03-27

PRIOR FILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-11

PRIOR FILING DATE: 1998-01-14

PRIOR FILING DATE: 1998-01-14

PRIOR FILING DATE: 1999-10-14

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENTED NOS: 44

SOFTWARE: PATENTED NOS: 44

SERVING NOS: 44
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                                                                                                                                                                                                                                                        Query Match 100.0%; Score 53; DB 14; Length 10; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 10; Conservative 0; Mismatches 0; Indels
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Fatent No. US20020058038A1
GENERAL INFORMATION:
FAPPLICANT: NICOLECTE, Charles A.
TITLE OF INVENTION: THERAPBUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: GZ 209500
CURRENT APPLICATION NUMBER: US/09/812,079A
CURRENT APPLICATION NUMBER: 60/191,050
FRIOR APPLICATION NUMBER: 60/191,050
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-12-12
FRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                TYPE: PRT
ORGANISM: Human cytomegalovirus
        PRIOR FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 43
SOFFWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 10; Conservative
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Gonczol, Eva
Berencsi, Klara
Kari, Caba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
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APPLICANT: Nicolette, Charles A.

TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS COMPOUNDS
FILE REPERENCE: 5018C
CURRENT APPLICATION NUMBER: US/10/434,982
CURRENT FILING DATE: 2003-05-10
PRIOR PLICATION NUMBER: US 09/812,079
PRIOR PLICATION NUMBER: US 60/191,050
PRIOR PLICATION NUMBER: US 60/191,050
PRIOR PLILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i Sequence 6, Application US/10223538
i Publication No. US20030120060A1
i GENERAL INFORMION:
APPLICANT: The Wistar Institute of, Anatomy & Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19477
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
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Mypothetical 16.7K protein - chrysanthemum virus B C;Species: chrysanthemum virus B C;Species: chrysanthemum virus B C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993 C;Accession: JQ1252 R;Levay, K.; Zavriev, S. J. Gen. Virol. 72, 2333-2337, 1991 A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of chrysant A;Reference number: JQ1246; MJID:92013948; PMID:1919520
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
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A;Nocaule type: DNA
A;Residues: 1-180
A;Cross-references: GB:AE008917; PIDN:AAL51519.1; PID:g17982235; GSPDB:GN00190
A;Cross-references: strain 16M
C;Genetics: A;Genetics: A;Ge
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Matches 6; Conservative
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54 SPRILGGG 61
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RESULT 49
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hypothetical protein 2 - fruit fly (Drosophila melanogaster)
()Species: Drosophila melanogaster
()Species: Drosophila melanogaster
()Date: 2.3-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
()Accession: S55017
()R;Bergstrom, D.E.; Merli, C.A.; Cygan, J.A.; Shelby, R.; Blackman, R.K.
()A.Title: Regulatory autonomy and molecular characterization of the Drosophila out at first A;Reference number: S55016; MUID:95286060; PMID:7768442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T36374
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
A;Accession: T36374
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A; Residues: 1-147 <OLI>
A; Cross-references: EMBL:AL049628; PIDN:CAB40863.1; GSPDB:GN00070; SCOEDB:SCE94.14
A; Experimental source: strain A3(2)
C; Genetics:
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                         A;Residues: 1-125 <STO>
A;Cross-references: GB:AE002093; NID:g4417270; PIDN:AAD20395.1; GSPDB:GN00139
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C.Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 03-Dec-1999
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C,Superfamily: Arabidopsis thaliana hypothetical protein T22F8.240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 62.3%; Score 33; DB 2; Length 125; Best Local Similarity 75.0%; Pred. No. 76; Matches 6; Conservative 1; Mismatches 1; Indels
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A;Molecule type: DNA
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A,Cross-references: FlyBase:FBgn0011818
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A; Residues: 1-154 <BER>
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                                                                                                                   A; Status: preliminary A; Molecule type: DNA
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                                                                                     A; Accession: G84604
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A, Gene: At2g21750
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A;Title: Expression of recombinant mouse/human chimeric antibody specific to human GMP-1
A;Reference number: JC2269; MUID:94334310; PMID:7520038
A;Accession: JC2270
A;Molecule type: mRNA
A;Residues: 1-113 «KUR»
A;Accession: PC2187
                                                                                                                                                                                                                                                                                                                                                                            C; Accession: 138740

Y. Ruff.—Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A; Title: Heavy and light chain variable region sequences and antibody properties of anti
A; Reference number: A38740; MUID:91177923; PMID:1706720

A; A; Accession: 138740

A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: JC2270; PC2187
                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Oct-1991 #Bequence_revision 18-Oct-1991 #text_change 21-Jan-2000
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A;Residues: 1-21 «KU2>
A;Rxperimental source: hybridoma cell
C;Comment: This protein is specific to human P-selectin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-101/Region: V segment
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A,Residues: 1-111 <RUF>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>
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Pred. No. 68;
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                                                                                                                                                                                                                                                        Ig kappa chain V region (Py42) - mouse C; Species: Mus musculus (house mouse)
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Best Local Similarity 75.v.
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97 TPRTFGGG 104
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Ig kappa chain V region (2GB) - mouse C; Species: Mus musculus (house mouse) C; Species: Musculus S; Say Sequence revision 18-Oct-1991 #sequence revision 18-Oct-1991 #sequence R; R; Ruff-Jamison, S; Campos-Gonzalez, R; Glenney Jr., J.R. J. Biol. Chem. 266, 6607-6613, 1991 A; Title: Heavy and light chain variable region sequences and antibody properties of anti-A; Reference number: A38740; MUID: 91177923; PMID: 1706720
                                                                                                                                                                                                                                                              A,Residues: 1-3300 <COL>
A,Cross-references: GB:295324; GB:AL123456; NID:g3261760; PIDN:CAB08587.1; PID:e1299834;
A,Experimental source: strain H37Rv
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holrcyd, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors. Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70575
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                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell receptor J-alpha wnII.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
Modecule type: mRNA
A;Residues: 1-23 <PLA>
A;Cross_references: EMBL:X71026; NID:g506575; PIDN:CAA50343.1; PID:g510308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>
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C; Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 75.0%; Pred. No. 68;
Matchés 6; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: $47208
K;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A;Reference number: $40133
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 66...,
-hea 6; Conservative
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Best Local Similarity
6, Conserve
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                                                                                                                                                                                                                                                                       A38149
RNA-directed RNA polymerase (EC 2.7.7.48) - yeast (Saccharomyces cerevisiae) RNA replicd
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S;Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25858
                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C;Accession: A38149; S27454
C;Accession: A38149; S27454
J. Biol. Chem. 267, 10874-10881, 1992
A;Title: T double-stranded RNA (deRNA) sequence reveals that T and W dsRNAs form a new FA;Reference number: A38149; WUID:92268145; PMID:1587863
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70575
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
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A;Residues: 1-940 coFF>
A;Cross-references: EMBL:NB6595; NID:g4079660; PIDN:AAC98708.1; PID:g4079661
A;Cross-sequence extracted from NCBI backbone (NCBIN:103889, NCBIP:103891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Molecule type: DNA
A;Residues: 1-1844 <SCH>
A;Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.20
A;Experimental source: BAC clone B23111; strain OR74A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related to Nup98-Nup96 precursor [imported] - Neurospora crassa
N/Alternate names: protein B23111.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.2%; Score 34; DB 2; Length 940; Best Local Similarity 66.7%; Pred. No. 3.6e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                   2; Indels
        66.7%; Pred. No. 1.7e+02;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: nucleotidyltransferase
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Best Local Similarity 75.00,
                                   Conservative
                                                                                                                                                  126 PKVDGGGPM 134
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                                                                                            2 PRVTGGGAM 10
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     Best Local Similarity
Matches 6; Conserv
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Cispecies: Arabidopsis thaliana (mouse-par cress)
Cispecies: Arabidopsis thaliana (mouse-par cress)
Cispecies: Arabidopsis thaliana (mouse-par cress)
Cispace: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., T., T., I.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Lile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: G90481
R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genlamk, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-4008 <COL>
A.Cross-references: GB:Z74024; GB:AL123456; NID:G3250700; PIDN:CAA98377.1; PID:e1301025;
C.Genetics:
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C;Genetics:
A;Gene: SS03008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenase, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
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Best Local Similarity 60.0%
6, Conservative
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Best Local Similarity 55.v.
For 5; Conservative
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A;Residues: 1-409 <KUR>
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A; Status: preliminary
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A;Map position: 1
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                                      C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C; Accession: P55101
R; Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. A; Holt, I.E. A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70252
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Deltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Hawlin, R.; Holroyd, S. Mature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-380 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75007.1; PID:g14972353; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Jitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: G97969
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-380 <KUR>
A; Cross-references: GB: AB007317; PIDN: AAK99587.1; PID:g15458380; GSPDB:GN00174
C; Genetics:
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C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C.Accession: G97959
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
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                                   03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
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C, Superfamily: nitrogen fixation protein nifS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: nitrogen fixation protein nifS
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75.0%;
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Best Local Similarity 75.00,
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221 TPLLTGGG 228
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Matches 6; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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A,Molecule type: genomic RNA
A,Residues: 1-380 <ROC>
A,Residues: 1-380 <ROC>
A,Cross-references: GB:M25270; NID:g323338; PIDN:AAA42904.1; PID:g323341
C;Comment: The genome is a single-stranded, positive-sense RNA. It codes for 33K, 92K, 4(
are core proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rigodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title; Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein AGR_C_764 [imported] - Agrobacterium tumefaciens (strain C58, Cereor C,Species: Agrobacterium tumefaciens
C,Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE007869; PIDN: AAK86246.1; PID: 915155352; GSPDB: GN00169
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R, Rochon, D.M.; Tremaine, J.H.
Wirology 169, 251-259, 1989
A, Title: Complete nucleotide sequence of the cucumber necrosis virus genome.
A, Reference number: A94391; MUID:89204896; PMID:2705296
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
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                                                                               Query Match 64.2%; Score 34; DB 2; Length 370; Best Local Similarity 85.7%; Pred. No. 1.46+02; Matches 6; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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A,Gene: AGR C 764
A,Map position: circular chromosome
    A; Map position: circular chromosome
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Matches 5; Conservative
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TPSISGGGTI 327
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Cjoate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
Cjoate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
Cjoacession: AH2629
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uricase - Deinococcus radiodurans (strain R1)
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A;Experimental source: strain Rl
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A,Experimental source: strain C58 (Dupont)
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64.2%; Score 34; DB 2; Length 288;

Best Local Similarity 55.6%; Pred. No. 1.1e+02;

Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                          A;Map position: 4
A;Introns: 57/3; 96/3; 153/3; 224/3
A;Note: F2009.200
C;Superfamily: erythrocyte band 7 integral membrane protein
A;Molecule type: DNA
A;Residues: 1-288 <BEV>
A;Cross-references: EMBL:AL021749
A;Experimental source: cultivar Columbia; BAC clone F2009
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87.5%;
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Best Local Similarity 87.5:
Matches 7; Conservative
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A,Map position: 1
C,Superfamily: urate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PRVTGGGAM 10
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7 PKIPGGGAI 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PRVTGGGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-298 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
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A;Gene: dcd
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RESULT 25

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Ridlaer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Litle: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                  Glacession: ABII14
RGlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, B.; Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A.; Johnes, L.M.; Karst, U.; Schooler, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: ABIO77; WUID:21537279; PMID:11679669
A.; Reference number: ABIO77; WUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxyethylthiazole kinase (ThiM) homolog lin0341 [imported] - Listeria innocua (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: lin0341
C;Superfamily: hydroxyethylthiazole Kinase; hydroxyethylthiazole Kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Superfamily: hydroxyethylthiazole kinase; hydroxyethylthiazole kinase homology
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1.269 < GLA>
A, Residues: GB: AL592022; PIDN: CAC95574.1; PID: g16412770; GSPDB: GN00178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AF1475
                      C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Lews-r
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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55.6%;
Species: Listeria monocytogenes
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Best Local Similarity 55.6'
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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C;Species: Ralobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84233
C;Accession: A84233
C;Accession: A84233
C;Accession: A84234
C;Accession: A84234
C;Accession: A84234
C;Accession: A84160; MulD:20504483; Ph.; Omer, A.D.; Ebhardt, H.D.; Lasky, S
Judy, W.V.; Rennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Judy, K.H.; Alam, M.; Freitas, T.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Judy, K.H.; Alam, M.; Freitas, T., Demnis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MulD:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                         hypotherical protein BH1384 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Accession: H8382.

R; Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A; Reference number: A83650; MuID:20512882; PMID:11058132
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A,Experimental Bource: strain C-125
C;Genetics:
A,Gene: BH1384
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; Length 252;
Pred. No. 99;
2; Mismatches 1; Indels
                                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                    1; Indels
                                                                                           DB 2;
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                                                                                        Score 34; DB Pred. No. 97; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.2%;
                                                                                                                     75.0%;
A; Cross-references: SGD:S0003029
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les 6; Conservative
                                                                                                                     Best Local Similarity 75.0 Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-267 <STO>
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A; Regidues: 1-252 <STO>
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                                  A; Map position: 7L
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Best Local 9
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RESULT 26

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Matches

RESULT 27

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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 1-3643 <SAU>
A,Residues: 1-3643 <SAU>
A,Cross-references: EMBL:AL109974; PIDN:CAB53322.1; GSPDB:GN00070; SCOEDB:SCF34.11c
A,Experimental source: strain A3(2)
C,Genetics:
A,Genetics:
A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Gene
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A;Cross-references: EMBL:Z72583; NID:g1322563; PID:e243286; PID:g1322564; GSPDB:GN00007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T49671
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49671
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N;Alternate names: hypothetical protein G3432
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: $64065
R;Feurmann, M.; Potier, S.; Souciet, J.L.
A;Reference to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
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A,Experimental source: BAC clone B8B20; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.0%; Score 35; DB 2; Length 3643; Best Local Similarity 85.7%; Pred. No. 8.7e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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A,Map position: 6
C,Superfamily: Neurospora crassa hypothetical protein B8B20.250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein B8B20.250 [imported] - Neurospora crassa
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Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-211 <SCH>
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R; Connor, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Natalandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUID:98295987; PMID:9634230
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A.Experimental source: strain H37Rv
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S;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross references: EMBL: Z50046; NID: 9899393; PIDN: CAA90368.1; PID: 9899395; MIPS: YDR145w; Experimental source: strain AB972
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A;Molecule type: DNA
A;Residues: 1-923 <COL>
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C, Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                            hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD8358.02
C;Species: Saccharomyces cerevisiae
C;Species: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%; Score 35; DB 2; Length 539; 66.7%; Pred. No. 1.4e+02; tive 1; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Gene: SGD:TAF61
A)Cross-references: SGD:S0002552; MIPS:YDR145w
A;Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                          R.Murphy, L.; Richards, C.; Harris, D. submitted to the EMBL Data Library, July 1995
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        470 PRVSGGG 476
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A; Residues: 1-539 <MUR>
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hypothetical protein [imported] - Arabidopsis thaliana hypothetical protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86228
C;Accession: H86228
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes B.; Hulzar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
A;Ritle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 4
A;Amp position: 4
A;Antrons: 19/1; 183/3; 239/2; 364/3; 394/1; 447/2
C;Antrons: 19/1; 9lucosylceramidase
C;Keywords: glycoprotein; glycosidase; hydrolase; lysosome; membrane bound; sphingolipid
E;1-21/bonain: signal sequence #status predicted <81G>
F;22-522/Product: glucosylceramidase #status predicted <APT>
E;22-522/Product: glucosylceramidase #status predicted <APT>
E;42,86,90,274,428/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL031254; PIDN:CAA20283.1; GSPDB:GN00022; CESP:F11E6.1
A;Experimental source: clone 4R79
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A;Molecule type: DNA
A;Residues: 1-522 <MI2>
A;Cross-references: EMBL:281058; PIDN:CAB02924.1; GSPDB:GN00022; CESP:F11E6.1
             glucosylceramidase (EC 3.2.1.45) precursor - Caenorhabditis elegans C,Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T18583; T20789
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85.7%; Pred. No. 1.3e+02;
iive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-522 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                submitted to the EMBL Data Library, August 1998
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Matches 6; Conservative
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Matches 7; Conservative
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A;Accession: T20789
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A;Accession: T18583
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C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: JC7280
R;Hixoyama, T.; Iwama, A.; Morita, Y.; Nakamura, Y.; Shibuya, A.; Nakauchi, H.
Biochem. Biophys. Res. Commun. 272, 224-229, 2000
A;Title: Molecular cloning and characterization of CRLM-2, a novel type I cytokine reception of CRLM-1.
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <ARN>
A:Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36611.1; PID:g498211
A:Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A53138
R;Del Sal, G.; Collavin, L.; Ruaro, M.E.; Edomi, P.; Saccone, S.; della Valle, G.; Schne Proc. Natl. Acad. Sci. U.S.A. 91, 1848-1852, 1994
A;Title: Structure, function, and chromosome mapping of the growth-suppressing human hom A;Reference number: A53138; MUD:94173926; PMID:8127893
A;Accession: A53138
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
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A;Remidues: 1-345 <RES>
A;Cross-references: GB:L13698; NID:g472859; PIDN:AAA72368.1; PID:g472860
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                                                                                                                                                                                                                                                                                                                   Query Match 66.0%; Score 35; DB 2; Length 336; Best Local Similarity 75.0%; Pred. No. 86; Matches 6; Conservative 2; Mismatches 0; Indels
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Pred. No. 92;
0; Mismatches
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hes 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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148 PRTSGGGA 155
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280 RLTGGGAL 287
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A; Residues: 1-359 < HIR>
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Query Match

Matches

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Cispecies: Agrobacterium tumefaciens
Cispecies: Assertium tumefaciens
Ridocher, B., Hinkle, G., Gattung, S., Miller, N., Blanchard, M., Qurollo, B., Goldman, A., Liu, F., Wollam, C., Allinger, M., Doughty, D., Scott, C., Lappas, C., Markelz, B., Aritle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume Arreference number: A97359; MUID:21608551; PMID:11743194
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ
A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                              R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle Karry, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
       conserved hypothetical protein Atu2585 [imported] - Agrobacterium tumefaciens (strain C56 C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-223 «KUR»
A; Cross-references: GB: AE008688; PIDN: AAL43566.1; PID: 917741080; GSPDB: GN00186
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72243
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Best Tocal 7; Conservative
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                                                                                                                         C; Accession: AH2893
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A;Gene: Atu2585
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                                                                                                                                                                                                                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) IIb - maize
NyAlternate names: starch branching enzyme IIb
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 18-Jun-1999
C;Accession: T01663
R;Kim, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.
R;Kim, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.
A;Bescription: Molecular cloning and characterization of the amylose-extender gene encod A;Reference number: Z14387
A;Accession: T01663
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C;Superfamily: 1,4-alpha-glucan branching enzyme
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
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A;Experimental source: strain B73
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C;Dacte: 24-Mar-1999 #text_change 18-Jun-1999
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999
C;Accession: T02981
R;Fisher, D.K.; Boyer, C.D.; Hannah, L.C.
Plant Physiol. 102, 1045-1046, 1993
A;Title: Starch branching enzyme II from maize endosperm.
A;Reference number: Z14808; MUID:94105320; PMID:8278524
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A;Residues: 1-799 - FFIS>
A;Cross-references: EMBL:LO8065; NID:g168482; PIDN:AAA18571.1; PID:g168483
A;Experimental source: cultivar W64AX182E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.9%; Score 36; DB 2; Length 799; Best Local Similarity 85.7%; Pred. No. 1.3e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 85.74
G; Conservative
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134 RITGGGAI 141
3 RVTGGGAM 10
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RESULT 13

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A;Residues: 1-788 <AQF>
A;Cross-references: GB:AE000748; NID:g2983960; PIDN:AAC07512.1; PID:g2983965; GB:AE000655; A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Vysotskaia, V.S.; Schwartz, J.R.; Kwan, A.; Toriumi, M.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:9819666; PMID:9537320
A,Accession: C70441
                                                                                                                                                                                                                              A; Cross-references: EMBL: AL023496; NID: e1292348; PID: e1292360; PIDN: CAA18910.1
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T13D8.31 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 10-Dec-1999
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A;Introns: 15/1; 70/1; 90/2; 145/3; 185/3; 217/2; 248/3; 292/3; 330/2
A;Note: T13D8.31
C;Superfamily: Saccharomyces hypothetical protein YDR531w
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                                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length 388;
Pred. No. 65;
2; Mismatches 0; Indels
R;Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1999
A;Reference number: Z20512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Reaidues: 1-404 <VYS>
A;Cross-references: EMBL:AC004473; NID:g3108025; PID:g3249085
                                                                                                           A,Accession: T28693
A,Status: prellminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-388 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Matches
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A; Residues: 1-254 <CAS.
A; Residues: 1-254 <CAS.
A; Cross=r-references: EMEL:W74162; NID:g146213; PIDN:AAA23909.1; PID:g146214
A; Cross=r-references: EMEL:W74162; NID:g16213; PIDN:AAA23909.1; PID:g146214
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: H65112
                                               gltF protein precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: S25281; H6512
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
A;Title: GitF, a member of the gltBDF operon of Escherichia coli, is involved in nitroge
A;Reference number: S25281; MUID:93078627; PMID:1447980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AE000401; GB:U00096; NID:g1789607; PIDN:AAC76246.1; PID:g1789608;
A,Experimental source: strain K-12, substrain MG1655
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A;Molecule type: DNA
A;Residues: 1-254 <BLAT>
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C.Species: Streptomyces coelicolor
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T28693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptomyces nogalater
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
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F;1.25/Domain: signal sequence #status predicted <SIG>
F;27-254/Product: gltF protein #status predicted <MAT>
F;213-229/Domain: transmembrane #status predicted <TMM>
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A;Experimental source: ATCC 27451
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R;Ylihonko, K.P.J.
submitted to the BMBL Data Library, October 1999
A;Reference number: Z23126
A;Accession: T46683
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2; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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1 TPRVTGGGAM 10

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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-85 < KUR>
A,Residues: 1-85 < KUR>
A,Residues: 1-85 < KUR>
A,Experimental Source: strain 1021, megaplasmid pSymA
A,Experimental Source: strain 1021, megaplasmid pSymA
B,Galibert, F.; Einan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, habbalt, P.; Värdembol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(Apritle: The composite genome of the legume symbiont Sincrhizobium meliloti.
A,Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: H95303
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse standard, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Suzzycki, R.; Wells, D.H.; Pah, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001
A;Ttle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilotials A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                    C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C87280
R;Niserman, W.C.; Fedlblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.!
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proco. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SMa0638 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                                                                                                                                         penicillin-binding protein, 1A family [imported] - Caulobacter crescentus
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Pred. No. 71;
0; Mismatches
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Best Local Similarity 81.0
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7; Conserve
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A; Residues: 1-653 <STO>
62 TPSVTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: H95303
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A;Gene: CC0252
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C; Species: Arabidopsis thaliana ($\text{Mouse-ear}$ cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Paccession: C56581
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.Y.; Hungles, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Ref. M.; Wu, D.; Yu, G; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Accession: C56581
A; Accession: C56581
                                                                                                                                                                                                                                                                                                            C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Accession: A46342; A39149
R;Pande, H.; Lee, T.D; Churchill, M.A.; Zaia, J.A.
Y;rology 178, 6-14, 1990
A;ritle: Structural analysis of a 64-kDa major structural protein of human cytomegalovin
A;Reference number: A46342; MUID:90357792; PMID:2167561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Human cytomegalovirus strain Towne pp65 gene: nucleotide sequence and expressid
A,Reference number: A39149; MUID:91220654; PMID:1850902
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                                                                                                                                                                                                                                                        65K lower matrix phosphoprotein - human cytomegalovirus (strain Towne)
N;Alternate names: 65K tegument protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 11-561 <PA2>
A;Cross-references: GB:M67443
A;Note: the authors translated the codon AAT for residue 478 as Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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100.0%; Pred. No. 0.076;
tive 0; Mismatches 0; Indel8
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Pred. No. 28;
0; Mismatches 1; Indels
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C;Superfamily: cytomegalovirus lower matrix phosphoprotein C;Keywords: matrix protein; phosphoprotein

A; Molecule type: DNA

A; Accession: A39149

Best Local Similarity 100. Matches 10; Conservative

Query Match

417 TPRVTGGGAM 426

RESULT 3

1 TPRVTGGGAM 10

ò g

A;Molecule type: protein A;Residues: 1-561 <PA1> R;Pande, H.; Campo, K.; Tanamachi, B.; Zaia, J.A. Virology 182, 220-228, 1991

A; Accession: A46342

RESULT 6

71.7%; 87.5%;

Query Match
Best Local Similarity 87.5-

A, Gene: F1511.14 A, Map position: 1

C;Genetics:

A.Status: preliminary A;Molecule type: DNA A:Residues: 1-383 <STO>

1 TPRVTGGG 8

C37855 B81009 B81009 B82031 A82834 A82834 A828415 T028415 T028415 T48228 H7137895 T732395 T733295 T733295 T733295 T733295 T732395 T733295 T733295 T733295 T733295 T733295 T732395 T732395 T732497 T735497 T736969 T736969 T736969 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T736985 T746085	C818 A6299 A7299 C876 C8486 C486 C486 C188 AG11 AG11 E309 E309 E309 E309 E863 C863 C863 C863 C863 C863 C863 C863
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## ALIGNMENTS

65K lower matrix phosphoprotein - human cytomegalovirus (strain AD169)

N;Alternate names: protein ULB3
C;Species: human cytomegalovirus, human herpesvirus 5
C;Dacession: A26793; SoB847
R;Rueger, B.; Klages, S.; Walla, B.; Albrecht, J.; Fleckenstein, B.; Tomlinson, P.; Barri J. Virol. 61, 446-453; 1987
A;Title: Primary structure and transcription of the genes coding for the two virion phosy A;Title: Primary structure and transcription of the genes coding for the two virion phosy A;Title: Primary structure and transcription of the genes coding for the two virion phosy A;Title: Primary structure and transcription of the genes coding for the two virion phosy A;Reference number: A93028; MUID:87112940; PMID:3027374
A;Residues: 1-561 <RUE>
A;Residues: 1-561 <RUE>
A;Residues: 1-561 <RUE>
A;Residues: Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; F. M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Reference number: G09749; MUID:90269039; PMID:2161319
A;Genesion: S09847

A;Status; nucleic acid sequence not shown, translation not shown A;Molecule type: DNA

A;Residues: 1-561 <CHE>
A;Residues: 1-561 <CHE>
A;Cross-references: EMBL:X17403; NID:959591; PIDN:CAA35357.1; PID:91780861
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:

A;Introns: 93/3 C;Superfamily: cytomegalovirus lower matrix phosphoprotein C;Keywords: matrix protein; phosphoprotein

Gaps . Match 100.0%; Score 53; DB 1; Length 561; Local Similarity 100.0%; Pred. No. 0.076; les 10; Conservative 0; Mismatches 0; Indels Query Match Best Local Si Matches 10;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 7, 2004, 13:01:12; Search time 20 Seconds (without alignments) 48.096 Million cell updates/sec Run on:

Title: Perfect score:

US-10-697-055-7 53 1 TPRVTGGGAM 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 10% Maximum Match 100% Listing first 500 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	65K lower matrix p	65K lower matrix p	hypothetical prote		hypothetical prote	gltF protein precu	probable lipoate p	hypothetical prote	hypothetical prote	lipoate-protein li	1,4-alpha-glucan b	1,4-alpha-glucan b	conserved hypothet	hypothetical prote	rod shape-determin	gas1 homolog - hum	cytokine receptor-	=			hypothetical glyci	➣	hypothetical prote			hypothetical prote	hydroxyethylthiazo		prohibitin-like pr
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	Query Match	100.0	100.0	71.7	69.8	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	99					64.2	64.2	64.2
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T1N6.24 protein -

ribosomal protein hypothetical prote hypothetical prote

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FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).

SQ SEQUENCE 142 AA; 15756 MW; 5459FD6B0BEAE21 CRC64;

Query Match 60.4%; Score 32; DB 1; Length 142;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 3 RVTGGG 8 |||||| | bb 67 RVTGGG 72 | Search completed: March 7, 2004, 13:03:18 | Job time: 26 secs Page 31

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delaveau T., Jacq C., Perea J.; "Sequence of a 12.7 kb segment of yeast chromosome II identifies a PDR-like gene and several new open reading frames."; Yeast 8:761-768(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; 20000103; SIA1:
GO; GO:0006885; C:actin cortical patch (sensu Saccharomyces); IDA.
GO; GO:0008092; F:cytoskeletal protein binding; IMP.
GO; GO:0007015; P:actin filament organization; IMP.
GO; GO:0007047; P:actin filament organization; IMP.
GO; GO:0006897; P:endocytosis; IMP.
GO; GO:0007121; P:polar budding; IMP.
                                                                                                                                                                                                         STRAIN=DDY 228;
WEDLINE-93328/65; PubMed-8335689;
Holtzman D.A., Yang S., Drubin D.G.;
"Synthetic-lethal interactions identify two novel genes, SLAI and
SLA2, that control membrane cytoskeleton assembly in Saccharomyces
                                                                                                                           Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                 01-OCT-1993 (Rel. 27, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Cytoskeleton assembly control protein SLA1. SLA1 OR YBL007C OR YBL0321.
           PRT; 1244 AA
                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Interacts with LSB5.-!- SIMILARITY: Contains 3 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93070613; PubMed=1441753;
                                                                                                                                                                                                                                                                                   cerevisiae.";
J. Cell Biol. 122:635-644(1993).
                                          (Rel. 27, Created)
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EMBL, Z35768, CAA84826.1; -.
EMBL, S47695, AAB23985.1; -.
PIR, S2527; S25327.
HSSP, Q03526, LAWJ.
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Pfam; PF03983; SHD1; 1.
PRINTS; PR00452; SHD0AAIN.
Procom; PD0000066; SH3; 3.
SWART; SM00326; SH3; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH LSB5.
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                                                                                                                                                              NCBI_TaxID=4932;
                                            01-OCT-1993
              SLA1_YEAST
SLA1_YEAST
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Langkjaer R.B., Cliften P.F., Johnston M., Piskur J.;
Langkjaer & B., Cliften P.F., Johnston M., Piskur J.;
"Yeast genome duplication was followed by asynchronous differentiation
of duplicated genes.";
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces exiguus (Yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 421:848-852(2003).
-!- SIMILARITY: Belongs to the S9P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                  ..
                                                            16 X 7 AA APPROXIMATE REPEATS OF
                                                                                                                                                                                                                                                                                                                     62.3%; Score 33; DB 1; Length 1244; 66.7%; Pred. No. 3.1e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                             1244 AA; 135848 MW; 7FD85AA776407624 CRC64;
            SH3 domain; Repeat.
SH3 1.
SH3 2.
SH3 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q876B4; Q876B5; Corrected) 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 110-0CT-2003 (Rel. 42, Last annotation update) 40S ribosomal protein S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PinerPro: IPR000754; Ribosomal S9.

Pfam; PF00380; Ribosomal S9; 1.

ProDom; PD001627; Ribosomal S9; 1.

PROSITE; PS00360; RIBOSOMAL S9; 1.

Ribosomal protein; Acetylatla; 0.

INIT MET 0.

INIT MET 0.
                                                                           T-G-G-A-M-M-P
                                                                                                                                                                                                         125.
135.
136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY144901; AAO32465.1; -. EMBL; AY144900; AAO32464.1; -.
 PRQSITE; PS50002; SH3; 3.
Cytoskeleton; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      1062 POVIGGAMM 1070
                                                                                                                                                                                                         1071
1090
1135
1161
1161
1176
1191
                                                                                                                                         951
1009
1026
1037
1037
                                                                                                                                                                                                                                                                                                                                                                              2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=34358;
PROSITE; PS50002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CBS 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS16 SACEX
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                            Query Match
                                                    DOMAIN
                                                                                                                                                        REPEAT
REPEAT
                            DOMAIN
                                        DOMAIN
                                                                                          REPEAT
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                                                                                                      REPEAT
                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 50
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PRT; 1093 AA.

STANDARD;

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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                    Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.; Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.; "Nucleotide sequence analysis of the gene encoding the Deinococcus radiodurans surface protein, derived amino acid sequence, and complementary protein chemical studies."; J. Bacteriol. 169:5216-5223(1987)
-! FUNCTION: Shape maintenance, possible protection from noxious enzymes or exogenous and unsettling DNA, and may mediate homotypic cell.cell contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry.

PTM: CONTAINS TIGHTLY BOUND REDUCING SUGARS (SIX PER POLYPEPTIDE CHAIN) AND FATTY ACIDS (COVALENTLY BOUND AND LOCATED IN THE N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERMINAL REGION).

THE THE NATIONAL REGION IN AROMATIC TERMINAL REGION RICH IN AROMATIC MISCELLANDEOUS: THE HYDROPHILIC C-TERMINAL REGION COLL SERVE TO AND THE AD COULD BE ENGAGED IN INTERACTIONS WITH NUCLEIC ACIDS, AND THE BOUND FATTY ACIDS AND THE N-TERMINAL REGION COULD SERVE TO ANCHOR THE LAYER TO THE OUTER MEMBRANE OF D. RADIODURANS. HDI LAYER CONTAIN ABOUT 30% BETA STRUCTURE AND VIRTUALLY NO ALPHA HELIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEXAGONALLY PACKED INTERMEDIATE-LAYER SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                           01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hexagonally packed intermediate-layer surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.3%; Score 33; DB 1; Length 1036; 60.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 RICH IN AROMATIC AA (29%).
108028 MW; AAFF98206A74AEEE CRC64;
                                                                                                                                                          Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; UNKNOWN 1.
Glycoprotein; Lipoprotein; Signal; Cell wall; S-layer.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER/THR-RICH (29%).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                              MEDLINE=88032846; PubMed=3667529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M17895; AAA23335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275
754
250
1030
                                                                                                                                               Deinococcus radiodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                        NCBI_TaxID=1299;
             HPI2_DEIRA
P13126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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SEQUENCE
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HPI2_DEIRA
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MEDLINE=94336695, PubMed=8058765;

MEDLINE=94336695, PubMed=8058765;

MEDLINE=94336695, PubMed=8058765;

Muchaer K., Berger R., Croce C.M., Canaani B.;

Huebner K., Berger R., Croce C.M., Canaani B.;

"Leucine-zipper dimerization motif encoded by the AF17 gene fused to reconstruct acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 91:8107-8111(1994).

-!- SIDCELLUIAR LOCATION: Nuclear (Potential).

-!- SIDCELLUIAR LOCATION: Nuclear (Potential).

-!- DISEASE: Involved in acute leukemias through a chromosomal translocation t(11;17)(q23;q21) that involves MLL/HRX and MLTG.

-!- SIMILARITY: Contains 2 PHD-type zinc fingers.

-!- SIMILARITY: HIGH, TO ARIO.

-!- SIMILARITY: HIGH, TO ARIO.

-!- SIMILARITY: HIGH, TO ARIO.

-!- SIMILARITY: HIGH. TO ARIO.

-!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

WWW="http://www.infoblogen.fr/services/chromcancer/Genes/AF17.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O. GO:006355; P:regulation of transcription, DNA-dependent; TAS. InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 1.
PR00249; PHD; 1.
PR071TS; PS01259; ZF PHD 1; 1.
PROSITE; PS01016; ZF PHD 1; 1.
PROSITE; PS01016; ZF PHD 2; 2.
Nuclear protein; Zinc-finger; Repeat; Chromosomal translocation;
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLL FUSION POINT (IN ACUTE MYELOID
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0
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Pred. No. 2.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F60042A6D3BF579E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEUKEMIA PATIENT)
                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHD-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHD-TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ALA.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.
GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1093 AA; 112021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U07932; AAA21145.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:7138; MLLT6.
MIM; 600328; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 SPHVTGSGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPRVTGGGA 9
                                                                                                                 Homb sapiens (Human).
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proto-oncogene.
ZN FING 5
ZN FING 51
ZN FING 117
DOMAIN 190
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                 AF-17 protein.
MLLT6 OR AF17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; 138533;
AF17_HUMAN
P55198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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879 TPNVTGNSAL 888

AF17_HUMAN

RESULT 48

1 TPRVTGGGAM 10

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RC STRAINCEV. Columbia;

RX MEDLINE=20083488; PubMed=10617199;

RADINE=20083488; PubMed=10617199;

RADINE=20083488; PubMed=10617199;

RADINE=20083488; PubMed=10617199;

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn M.,

RA Pohl T., Duesterhoeft A., Stiekema W., Schmidtheini T.,

RA Weichsel J., Zimmermann W., Watlen B., Mache R., Mueller M.,

RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Braeken M., Wellein J., Zimmermann W., Wedler H., Ridley P.,

RA Braeken W., Weltelm G., Ramsperger U., Hilbert H., Braun M.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkes W.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkes W.,

RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

RA Dereiser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,

Van Montagu M., Rogers U., Feldpausch M., Lennard N., McLay K.,

RA Dose S., de Haan M., Marse A.C., Schaefer M., Meller-Auer S.,

RA Borkova D., Bloecker H., Scharfe M., Gramderath K., Dauner D., Herzl A.,

RA Borkova D., Rolley R., Schaffe M., Gramder B., Piravandi E.,

RA Abbons T., Weber N., Vatale D., Liguori R., Piravandi S.,

RA Abbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Casacuberte E.,

RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Taron D., Jesse T.,

RA Perskman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Frishman D., Haber S., Denner B., Denner D., Stocker S.,

RA Berder P. R., Reigher B., Bent E., Men Bertie B., Paller S., Paller B., Bent S., Reigher B., Bent S., Reigher B., Bent S., Reigher B., Bent S., Reigher B., Bent S., Reig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
Probable pantochenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantaa; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 62.3%; Score 33; DB 1; Length 807; Local Similarity 85.7%; Pred. No. 2e+02; ls Indels les 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                        Transferase, Serine/threonine-protein kinase, ATP-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                          138 138 BY SIMILARITY.
807 AA; 85231 MW; 66C274219155D091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE
                       Pfam; PF00069; pkinase; 1.
ProDom; PD00001; Prot_kinase; 1.
SWART; SM00564; PQQ; 4.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
InterPro, IPR008271; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AT4G32180 OR F10M6.180 OR F10N7.10
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                                                                                                                                                                                                                                                                                                                             272
30
44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNK1 ARATH STANDARD
Q8L5<u>Y</u>9; 049372; 049374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 PAVTGGG 661
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                                                                                                                                                                                                                                                                                                  Phosphorylation.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                     DOMAIN
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SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

Manada K., Lim U., Dale J.M., Chen H., Shinn P., Palm C.J.,

Rarlin-Newmann G., Liu S.X., Lam B., Sakann H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Eju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Chao Q., Choy N., Johnson-Hopson C., Hauan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajiwa M., Narusaka M., Saki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threaded J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Coutney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Tamer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Ramer J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Achen B., Marra M.A., Martienssen R., McCombie W.R., Lodhi M., Johnson A., Chen B., Marra M.A., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphopantothenate.
-!- ENZYME REGULATION: Regulated by feedback inhibition by malonyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
-!- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
-!- SIMILARITY: Belongs to the eukaryotic partotherate kinase family.
-!- CAUTION: Ref.1 sequences differ from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 302:842-846(2003).
-!- FUNCTION: Plays a role in the physiological regulation of the intracellular CoA concentration (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAM: JIGGO0555; pank eukar; 1.
Transferase; Kinase; ATP-Dinding; Coenzyme A biosynthesis.
SEQUENCE 870 AA; 96234 MW; 23CECA42A3D8EA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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EMBL, AL161580; CAB16936.1, ALT_SEQ.
EMBL, AL021636; CAA16571.1, ALT_SEQ.
EMBL, AX099839; AAM20690.1; -.
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InterPro; IPR004567; PanK_eukar.
Pfam; PF01937; DUF89; 1.
Pfam; PF03630; Fumble; 1.
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Best Local Similarity 85...
Fra 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:769-777(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsumoto A., Hong S.K., Ishizuka H., Horinouchi S., Beppu T., "Phosphorylation of the AfeR protein involved in secondary metabolism in Streptomyces species by a eukaryotic-type protein kinase."; Gene 146:47-56(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ueda K., Umeyama T., Beppu T., Horinouchi S.;
"The aerial mycelium-defective phenotype of Streptomyces griseus resulting from A-factor deficiency is suppressed by a Ser/Thr kinase of S. coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed R. P. Cardeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Rarper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Horneby T., Howarth S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of the model actinomycete Streptomyces
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
                                 Score 33; DB 1; Length 692;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumoto A., Hong S., Ishizuka H., Horinouchi S., Beppu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Umeyama T.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
692 AA; 76745 MW; 0E58310C4F3EFD80 CRC64;
                                                                                                                                                                                                                                  AFSK STRCO STANDARD; PRT; 799 AA. P54741; Q9F365; Q91002; D01-007-1996 (Rel. 34, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2003 (Rel. 42, Last annotation update) Serine/threconine protein kinase afsk (EC 2.7.1.37). AFSK OR SCO4423 QR SGF811.21 OR SCD6.01.
                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE=94341568; PubMed=8063104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96186909; PubMed=8635757;
                                     62.3%;
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Nature 417:141-147(2002)
                                                                          Conservative
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                                                                                                                                              513 TPNETGGG 520
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                                                                                                             1 TPRVTGGG 8
                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1902;
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     SEQUENCE
                                      Query Match
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                                                                            Matches
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and for commercial
                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: INVOLVED IN THE REGULATION OF SECONDARY METABOLISM BY PHOSPHORYLATING, ON BOTH SER AND THR, THE AFSR GLOBAL REGULATORY PROTEIN INVOLVED IN THE CONTROL OF SECONDARY METABOLISM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                   Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W; 4BE9BED4169F6F5B CRC64;
     Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine protein kinase afsk (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         807 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
      and this statement is not removed.
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                    entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                      Phossite; P54741; -.
InterPro; IPR00711; Ser thr pkin AS.
InterPro; IPR08271; Ser thr pkin AS.
Pfan; PF00069; pkinase; I.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                           Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PhosSite; P54742; -.
InterPro; IPR000719; Prot kinase.
                                                                                        AL939120; CAD55483.1; -.
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799 AA; 83787 MW;
                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                     EMBL; D45382; BAA08229.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 PAVTGGG 654
                                                                                                                                                                                         SM00564; PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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      modified
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVYGHHWRASTGDARSDCAPSPRIAPPGAPLALTAHPGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADTPETQDSVSSSRKPASA -> SLRPPLASLDRRRAFRLR
PQPSHRSPRGPSSPHCTPGCGLGRHAGDAGFGLQQSKASLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishigami A., Guerrin-Weber M., Sebbag M., Serre G., Senshu T.;
"Molecular cloning of peptidylarginine deiminase type I cDNA from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         citrulline + NH(3).
-!- COFACTOR: Requires calcium ions (By similarity).
-!- SIMILARITY: Belongs to the protein arginine deiminase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
LeCOT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last amontation update)
Protein-arginine deiminase type I (EC 3.5.3.15) (Peptidylarginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
S-palmitoyl cysteine (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the deimination of arginine residues of proteins (By similarity).
-!- CATALYTIC ACTIVITY: Protein L-arginine + H(2)0 = protein L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 33; DB 1; Length 561; 66.7%; Pred. No. 1.4e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                         CYTOPIASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B6537DCAD4F7BE27 CRC64;
                                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                            5 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                      GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561 AA; 59354 MW;
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Best Local Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Epidermis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human epidermis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                            60
76
413
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424
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PADII OR PDII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDI1 HUMAN
                                                                                                                                                                                                 DOMAIN
TRANSMEM
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                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 42
PDI1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATC 12228)."; Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the nascent protein chain from the A-site to the P-site of the
                                                                                                               ..
                                                                                Length 663;
Pfam; PF03068; PAD; 1.

Hydrolase; Calcium-binding; Multigene family.

CA BIND 506 517 BF-HAND (POTENTIAL).

SEQUENCE 663 AA; 74607 MW; 0BD8D460634EE2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGR00231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                62.3%; Score 33; DB 1; I
75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HANAB, ME 00054; -; 1.
InterPro; IRR000795; BF GTPbind.
InterPro; IRR0009025; BFG [II V.
InterPro; IRR009022; BFG [II V.
InterPro; IRR004161; BFFT D2.
InterPro; IRR004161; BFFT D2.
InterPro; IRR004161; BFFT D2.
InterPro; IRR009000; Translat_factor.
Pfam; PF00579; BFG C; 1.
Pfam; PF00164; BFG C; 1.
Pfam; PF00169; GFB EFT 1.
Pfam; PF00161; BFFT D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP
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                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last a
Elongation factor G (EF-G).
                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
                                                                                               Local Similarity 75.0 nes 6; Conservative
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
23
84
137
                                                                                                                                                                             415 SPPVTGGG 422
                                                                                                                                             1 TPRVIGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 12228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                         FUSA OR SE0311
                                                                                                                                                                                                                                                           EFG STAEP
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                                                                                 Query Match
                                                                                                                                                                                                                             RESULT 43
EFG_STAEP
                                                                                                               Matches
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bestow E.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkova D., Botchan M.R., Bouck J., Broketein P., Botter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P., Chartis R.D., Davier B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodlon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R., Gong T., Gong T., Gorg T., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003583; AAF51246.1; ALT_TERM.
EMBL; U63862; AAC47551.1; -
FlyBase; FBGn0011818; oaf
FO; GO: GO: GO: FEGRALE meiosis chromosome segregation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merli C., Bergstrom D.E., Cygan J.A., Blackman R.K., "Promoter specificity mediates the independent regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT FIRST PROTEIN.
AT FIRST SHORT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-89 FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO/SER/THR-RICH.
POLY-THR.
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POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96217926; PubMed=8675012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L31349; AAC37219.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighboring genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINES=9514877; PubMed=7815325; Co., Mosley M.J., Wilson K.H., Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H., Worman N.P., Campbell S., Fidock M.D., Furness L.M., Parry-Smith D.J., Peter B., Bailey D.S., "Cloning and pharmacological characterization of human alpha-1 adrenergic receptors: sequence corrections and direct comparison with
                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A., Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G., "Molecular cloning and expression of the cDNA for the alpha ladarenergic receptor. The gene for which is located on human
                                                                                    ;
0
                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00227; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
Cprocein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate. DOMAIN
                                               62.3%; Score 33; DB 1; Length 487; 66.7%; Pred. No. 1.2e+02; rive 1; Mismatches 2; Indels
413 413 A -> T (IN REF. 1).
487 AA; 53728 MW; FOD7A117BE358B3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley, TISSUE-Brain cortex;
MEDLINE-91177889, PubMed=1706716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Biol. Chem. 266:6365-6369(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL; M60654; AAA63477.1; -.
EMEL; Li3171; AAB65704.1; -.
PIR; A38731; A38731.
InterPro; IPRO00276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                              adrenergic receptor) (RA42).
ADRAID OR ADRAIA.
                                                                      Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                         373 TATITGGGA 381
                                                                                                                         1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
   CONFLICT
                                                                                                                                                                                                                                                ALAD RAT
                                                        Query Match
                                                                                                                                                                                                               RESULT 41
                                                                                                                                                                                                                                  AIAD RAT
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1 (POTENTIAL).

**TRANSMEM** 

CONFLICT

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                                                                                                                                                                                                                                                                                                                                                                MEDLINE-2238825; PubMed=12477932,

TISSUB-Bone marrow, and Muscle;

MEDLINE-2238825; PubMed=12477932,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Haders G.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Sarchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                               Semba S., Ouyang H., Han S.-Y., Kato Y., Horii A., "Analysis of the candidate target genes for mutation in microsatellite instability-positive cancers of the colorectum, stomach, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: INVOLVED IN CELL CYCLE ARREST WHEN DNA DAMAGE HAS
OCCURRED OR WHEN UNLIGATED DNA IS PRESENT. BINDS TO AND
PHOSPHORYLATES CDC25A, CDC25B AND CDC25C. PHOSPHORYLATION OF
CDC25C. CREATES A BINDING SITE FOR 14.3-3 PROTEIN WHICH INHIBITS
CDC25C. THIS PREVENTS ACTIVATION OF THE CDC2-CYCLIN B COMPLEX AND
PREVENTS MITOTIC ENTRY. PHOSPHORYLATES CDC25C ON SERINE-216.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed ubiquitously with the most abundant
expression in thymus, testis, small intestine and colon.
-!- THY: Phosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMI
                                                                                                                                                                                                                                     Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                  MEDLINE=20184068; PubMed=10717241;
                                                                                                                                                                        int. J. Oncol. 16:731-737(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF016582; AAC51736.1; -. EMBL; AF032874; AAB88852.1; -.
Curr. Biol. 7:977-986(1997)
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                          endometrium.
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BAA84577.1; JOINED. BAA84577.1; JOINED. BAA84577.1; JOINED.

AB032378; AB032379; AB032387;

EMBL; EMBL; EMBL; EMBL;

AB032377;

EMBL;

EMBL;

BAA84577.1;

JOINED. JOINED. JOINED. JOINED. JOINED.

BAA84577.1; BAA84577.1;

AB032380;

AB032381

BAA84577.1; BAA84577.1; BAA84577.1; BAA84577.1;

AB032385; 1

AB032383; AB032384;

EMBL;

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DR GK; Uttalong: TAS.

BR GO:0004672; F:protein Kinase activity; TAS.

GO: GO:0004672; F:protein Kinase activity; TAS.

BR GO: GO:000077; F:protein Kinase activity; TAS.

BR GO: GO:0000775; F:protein Kinase activity; TAS.

BR GO: GO:0000713; F:protein Kinase signal transduction re. .; TAS.

BR GO: GO:0000713; F:protein Kinase.

BR GO: GO:000079; P:regulation of Cell proliferation; TAS.

BR GO: GO:000079; P:regulation of Cell proliferation; TAS.

BR GO: GO:000079; P:regulation of Cell proliferation; TAS.

BR InterPro; IPR00229; Prot Kinase.

BR InterPro; IPR002290; Ser thr pkinase.

BR FFOOD FROM PROCONTISE SER THR PKINASE.

BR FROSTIE; PROFONISE TROFEIN KINASE ATP; 1.

BR FROSTIE; PROFONISE TROFEIN KINASE DOM; 1.

BR FROSTIE; PROFONISE TROFEIN KINASE DOM; 1.

BR Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; RW DNA damage; Nuclear protein; Phosphorylation; 3D-structure.

FT ACT SITE 130 BY SIMILARITY.

FT ACT SITE 130 BY SIMILARITY.

FT ACT SITE 130 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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MEDLINE=2019606; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=Berkeley, TISSUB=Embryo;
MEDLINE=55286060; PubMed=776842.
Bergetrom D.E., Merli C.A., Cygan J.A., Shelby R., Blackman R.K.,
"Regulatory autonomy and molecular characterization of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Neoptera, Endopteray, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxIb=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONLE DANGER STANDARD; PRT; 487 AA. (ONLESS). (ONLESS). (CT-2001 (Rel. 40, Last sequence update). (16-OCT-2001 (Rel. 40, Last sequence update). (16-OCT-2003 (Rel. 42, Last annotation update). Out at first protein [Contains: Out at first short protein]. OAF OR CG9884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 476; Pred. No. 1.2e+02; 0; Mismatches 1; Indels
EMBL; AF527555; AAM78553.1; -. EMBL; BC004202; AAH04202.1; -. EMBL; BC017575; AAH17575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                out at first gene.";
Genetics 139:1331-1346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%;
Local Similarity 85.7%;
les 6; Conservative 0
                                                         PDB; 1IA8; 18-APR-01.
Genew; HGNC:1925; CHEKI.
GK; 014757; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 PRVTSGG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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MEDLINE=87146423; PubMed=3029698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEKI OR CHKI.
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SEQUENCE
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CHK1_HUMAN
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N-LINKED (GLCNAC. .) (POTENTIAL).
MIQDPDSDQPLNSLDVKPLRKPRIPMETFRK -> MSNPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Shufflon protein B'.
Bscherichia coli.
Plasmid Incll R64, and Plasmid Incll Collb-P9.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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0
         R MIM; 606565; -. Gintegral to membrane; NAS. GO; GO:0016021; C:integral to membrane; NAS. GO; GO:0006502; F:serine-type endopeptidase activity; NAS. GO; GO:0006502; F:serine-type endopeptidase activity; NAS. R InterPro; IPR001903; Cys Ser trypsin.

R InterPro; IPR001031; LDL_receptor_A.

R InterPro; IPR001134; Peptidase_S1A.

R InterPro; IPR001190; SICI receptor.

R Pfam; PR001090; SICI receptor.

R Pfam; PR001091; LIDL_receptor.

R Pfam; PR001091; LIDL_RAS.

R MART; SM00202; CHYMOTRYPSIN.

R SMART; SM00202; SIN. 1.

R PROSITE; PS00203; LDLRA 2; FALSE NEG.

R ROSITE; PS00203; LDLRA 2; FALSE NEG.

R ROSITE; PS00203; TRYPSIN HIS; I.

R RROSITE; PS00135; TRYPSIN HIS; I.

R RROSITE; PS00135; TRYPSIN HIS; I.

R RROSITE; PS00135; TRYPSIN HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 437;
85.7%; Pred. No. 1.1e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease; Transmembrane; Signal-anchor. nowmin 1 32 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 AA; 48204 MW; 351B2FD4A8657B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPVSPWRPSES (IN REF. 2)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 TPRVVGG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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ACT_SITE
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                                                                                                                                                                                SEQUENCE OF 362-444 FROM N.A.
PLASMID=Incll Collb-P9;
MEDLINE=90160674; PubMed=2623084;
Kim S. R., Komano T.;
"Cloning and nucleotide sequence of the Collb shufflon.";
Plasmid 22::80-184(1989).
-!-MISCELLANBOUS: THIS PROTEIN IS EXPRESSED BY A SHUFFLON (=
-L-MISCELLANBOUS: THIS PROTEIN THAT WORKS AS A BIOLOGICAL SWITCH). THE
ORPS OF THIS REGION SHARE A CONSTANT N-TERMINUS, WHILE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98044285; PubMed-9382850;
Flaggs G., Plug A.W., Dunks K.M., Mundt K.E., Ford J.C.,
Quiggle M.R.E., Taylor B.M., Westphal C.H., Ashley T., Hoekstra M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97426625; PubMed=9278511;
Sanchez Y., Wong C., Thoma R.S., Richman R., Wu Z., Piwnica-Worms H.,
Elledge S.J.;
Komano T., Kubo A., Nisioka T.; "Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames."; Nucleic Acids Res. 15:1165-1172(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Science 277:1497-1501(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.3%; Score 33; DB 1; Length 444; 75.0%; Pred. No. 1.1e+02; rative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 444 VARIABLE REGION.
444 AA; 46945 MW; E5E517667FE46304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine-protein kinase Chkl (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONSTANT REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90039; BAA14091.1; -.
PIR; D26421; D26421.
InterPro; IPR007001; Shufflon_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB027308; BAA77987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04917; Shufflon N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TERMINUS IS VARIABLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 RVTGGGGI 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
FUNCTION: Probable protease. Seems to be capable of activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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0
                            -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- SIMILARITY: Belongs to peptidase family $1.
-!- SIMILARITY: Contains 1 LDL-receptor class A domain.
-!- SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 33; DB 1; Length 435; 85.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase, Serine protease, Transmembrane, Signal-anchor.
DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47495 MW; DC52E45A43E01369 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
BY SIMILARITY
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                                                                                                                                                                                                                                                                                                  nwuj, mul. 1.20040)
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR002172; LDL_receptor A.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR001124; Peptidase_S1.
InterPro; IPR001134; Peptidase_S1.
InterPro; IPR001190; Srcr_receptor.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00129; Trypsin; 1.
PROSITE; PS01209; LDLRA_1; PALSE_NEG.
PROSITE; PS01209; LDLRA_1; PALSE_NEG.
PROSITE; PS00420; SRCR_1; PALSE_NEG.
PROSITE; PS00420; SRCR_1; PALSE_NEG.
PROSITE; PS00420; SRCR_1; PALSE_NEG.
PROSITE; PS00430; SRCR_1; PALSE_NEG.
PROSITE; PS00430; SRCR_1; PALSE_NEG.
PROSITE; PS00135; TRYPSIN SIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                           EMBL; AY043240; AAK85307.1; -.
EMBL; BC021368; AAH21368.1; -.
HSSP; P00761; IAN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                          MGD; MGI:2384877; Tmprss4.
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203
81
81
181
191
308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          MEROPS; S01.034;
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ACT SITE
ACT SITE
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437 AA.

PRT;

TMS4 HUMAN STANDARD; 1 Q9NRS4; Q9NZA5; 16-OCT-2001 (Rel. 40, Created)

RESULT 37 TMS4 HUMAN

200 TPRVVGG 206

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC TISSUE-PROTECTES:

RA KEDLINE-22388257; PubMed=12477932;

RA KLausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat Chenkol., Marusina R., Farmer A.P., Rubin G.M., Hong L., Schaefer C.F., Rapletcon M.J., Uedin T.B., Toshiyuki S., Garninci P., Prange C.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Garninci P., Mullahy S.J.,

RA Bosak S.A., McEwan P.M., Scherger G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., McTley K.C., Hale S., Garcia A.M., Gabs R.A.,

RA Richards S., McTley D.M., Scdergren B.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

RA Pahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RAC (By similarity): Type II membrane protein (Potential):

C. --- FUNCTION: Probable protease. Seems to be capable of activating RAC (By similarity): Type II membrane protein (Potential):

C. --- SIMCELLULAR LOCATION: Type II membrane protein (Potential):

and ampullary cancer. Very weak expression in normal and ampullary concern. Farmilarity S.C.

---- SIMLARITY: Contains I BRCR domain.

C. --- SIMLARITY: Contains I BRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric, colorectal
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine
                                                                                                                                                                                                                                                                                                                                                                                                                                             Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.; "MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization.";
                                                                                                                                                                                                                                                                              Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B., Iwdmura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.; "A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer.";
                                                                                                                                  Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Pancreatic carcinoma;
MEDLINE-20283276; PubMed=10825129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF179224; AAF74526.1; --
EMBL; AF216312; AAF31436.1; --
EMBL; BC011703; AAH11703.1; --
HSSP; P00763; 1DPO-
MEROPS; S01.034; --
Genew; HGNC:11878; TMPRSS4.
                                                                                                                                                                                                                                                                                                                                                                                       Cancer Res. 60:2602-2606(2000).
                                                                               (MT-SP2).
                                                                                                                       Homo sapiens (Human)
                                                                          protease 2) (MT-SP2
TMPRSS4 OR TMPRSS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas;
                                                                                                                                                                                      NCBI_TaxID=9606;
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SEQUENCE FROM N.A.

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Bagni C., Mariottini P., Annesi F., Amaldi F.,
"Human ribosomal protein L4: cloning and sequencing of the cDNA and
primary structure of the protein.";
Biochim. Biophys. Acta 1216:475-478(1993).
                                                                                                                                                MEDLINE=21864036; PubMed=11875025; Kawasaki K., Kato S., Higa S., Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kenmochi N.; Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.; "The human ribosomal protein genes: sequencing and comparative
                                                                                                                        Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                           Bagni C.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X73974; CAA52154.1; -.
EMBL, L20868; AAA60281.1; ALT_SEQ.
EMBL, D23660; BAA04887.1; -.
            MEDLINE=94092742; PubMed=8268230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BC001365; AAH01365.1; EMBL, BC005817; AAH05817.1; -. EMBL, BC007259; AAH07259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC007996; AAH07996.1; -.
EMBL; BC009888; AAH09888.1; -.
EMBL; BC010151; AAH10151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC010151; AAH10151.1; -. EMBL; BC014653; AAH14653.1; -. EMBL; AB061820; BAB79458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC007748; AAH07748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-2DPAGE; P36578; HUMAN.
                                                                                                                                                                                      analysis of 73 genes.";
Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:10353; RPL4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T09551; T09551
                                                                                                                                              SECUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
                                                                                                             rissue≈Lymphoma;
                                                                  REVISIONS.
                                                                                                                     Kato S.;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
RACINESUSE STREATS, PubMed=12477932;

RADINELS 238257; PubMed=12477932;

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Dischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Halkeing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rahas A.C., Girimwood J., Schmutz J., Myers R.M.,

Radiriquez A.C., Girimwood J., Schmutz J., Myers R.M.,

Radiriquez A.C., Girimwood J., Schmutz J., Myers R.M.,

Radiriquez A.C., Girimwood J., Schmutz J., Myers R.M.,

Radensration and initial analysis of more than 15,000 full-length

T. "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                             ó
GKi, P36578; -.

MIM; 180479; -.

GO, GO:0005842; C:cytcosolic large ribosomal subunit (sensu Eu. . .; TAS. GO; GO:0003733; F:RNA binding; TAS.

GO; GO:0003735; F:RNA binding; TAS.

GO; GO:0006412; P:protein biosynthesis; TAS.

InterPro; IPR002136; Ribosomal_L4/L1E.

Pfam; PF00573; Ribosomal_L4; 1.

PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22144321; PubMed=12149280; Hummler E., Rossier B.C.; Wagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.; Synergistic activation of ENaC by three membrane-bound channel-activating serine proteases (McAPI, mCAP2, and mCAP3) and serum- and glucocorticoid-regulated kinase (SgK1) in Xenopus oocytes."; J. Gen. Physiol. 120:191-201(2002).
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Channel-activating protease_2) [mCAP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamhalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                    Length 427;
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36 36 1 -> M (IN REF. 1).

63 63 S -> R (IN REF. 1).

147 147 V -> F (IN REF. 1).

201 201 MISSING (IN REF. 1).

427 AA, 47697 MW, 4785ED31699CD792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 33; DB 1; I
85.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                      LYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                llarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                                                                                                                           Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPRSS4 OR CAP2
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SEQUENCE
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RPL4 OR RPL1.
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                                    Query'Match
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                                                                   Matches
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Stodingez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Matl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Matl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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o
                                                                                                                                                                                                                                                                                                                                                                                                 161 161 Y -> F (IN REF. 1; BAB27375).
419 AA; 47153 MW; E736E656A60BE85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 419; 85.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L4 (L1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL L1E; FALSE NEG.
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                          EMBL; AK008098; BAB25458.1; -.
EMBL; AK011068; BAB27375.1; -.
EMBL; BC003459; AAH03459.1; -.
MGD; MGI:1915141; 2010004723Rik.
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00573; Ribosomal_L4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X99909; CAA68182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 PRVRGGG 83
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Mongrel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sandholzer U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPL4 OR RPL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RL4 CANFA
Q28346;
                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINE-Sprague-Dawley, TISSUE-Liver,
MEDLINE-Sprague-Dawley, TISSUE-Liver,
MEDLINE-S6024571; PubMed=7575549;
Chan Y.-L., Olvera J., Wool I.G.;
"The primary structures of rat ribosomal proteins L4 and L41.";
Biochem. Biophys. Res. Commun. 214:810-818(1995).
-: SIMILARITY; Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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0
                                                                              62.3%; Score 33; DB 1; Length 420;
85.7%; Pred. No. 1e+02;
tive 0; Mismatches 1; Indels
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NON TER 1 1 SEQUENCE 420 AA; 47384 MW; D971FC2950A387BB CRC64;
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62.3%; Score 33; DB 1;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches
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01-JUN-1994 (Rel. 29, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RPL4 OR RPL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002136; Ribosomal L4/L1E.
Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYS-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X82180; CAA57671.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                        Best Local Similarity 85.7
Matches 6; Conservative
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96004470; PubMed=7551039; Reeves R.A., Bergquist P.L.; Munro G.K., McHale R.H., Saul D.J., Reeves R.A., Bergquist P.L.; Munro G.K., McHale R.H., Saul D.J., Reeves R.A., Bergquist P.L.; Agene encoding a thermophilic alkaline serine proteinase from Thermus sp. strain Rt41A and its expression in Escherichia coli."; Microbiology 141:1731-1738 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 92362605; PubMed=1499549;
Peak K., Daniel R.M., Monk C., Parker L., Coolbear T.;
Peak K., Daniel R.M., Monk C., Parker L., Coolbear T.;
Peak K., Daniel R.M., Monk C., Parker L., Coolbear T.;
Peak K., Daniel R.M., Monk C., Parker L., Coolbear T.;
Isolated from Thermus sp. strain Rt41A.";
Eur. J. Biochem. 207:1035-1044(1992)
-: FINCTION: THERMOSTMELE SERNINE PROTEINASE WITH PREFERRED
-: FINCTION: THERMOSTMELE SERNINE PROTEINASE WITH PREFERRED
-: SUBCELIULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: Contains 4 Cys residues that form two disulfide bonds.
-!- PTM: This proteinase has a 0.7% carbohydrate content.
-!- SIMILARITY: Belongs to peptidase family S8.
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                                                                                                                                                                                                                                                                                                                 62.3%; Score 33; DB 1; Length 408; B5.7%; Pred. No. 1e+02; tive 0; Mismatches 1; Indels
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01-DECT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Extracellular serine proceinase precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                           408 AA; 44869 MW; DAD8C75E8CDA7594 CRC64;
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InterPro; IPR000437; Prok lipoprot_S.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                           EMBL; AF134732; AAD32206.1; -.
InterPro; IPR002136; Ribosomal_L4/L1E.
PEAM; PF00573; Ribosomal_L4; 1.
PROSITE; PS00939; RIBOSOWAL_L1E; 1.
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HSSP; Q99405; 1MPT.
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Best Local Similarity 85...
Best Local 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             2 PRVTGGG 8
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                                                                                                                                                                                                                                                              Ribosomal protein.
SEQUENCE 408 AA;
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RE SEQUENCE FROM N.A.

RE STRAIN=CSTBL/66; TISSUE=Embryonic liver, and Small intestine;

RE MEDLINE=21085660; PubMed=11217851;

RA MARINESTBL/66; THATA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Iawa M., Nishi K., Konno H., Adachi J., Fukuda S.,

RA Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Mateuda H.A., Rabhurner M., Batalov S., Casavant T.,

RA Kadota K., Mateuda H.A., Rabhurner M., Batalov S., Casavant T.,

RA Schriml L., M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Mornstein M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hawashi Y., V.
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                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                               EXTRACELLULAR SERINE PROTEINASE.
                                                                                                                                                                                                                                                 62.3%; Score 33; DB 1; Length 408; 60.0%; Pred. No. 1e+02;
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        PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
SIGNAL 19
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
60S ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                      42284 MW;
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PRINTS; PR00723; SUBTILISIN.
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202
354
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Best Local Similarity
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131
169
169
202
354
354
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ACT_SITE
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Drosophila melanogaster (Fruit fly).

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Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C., Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., Darnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J., Richoff K., Toth K., King L., Bahret A., Miller B., Marra M.A., Antiensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I., Antiensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I., Britan K.-D., Terryn N., Hartley N., Bent B., Johnson S., Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W., Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W., Antizenegger U., Wedler H., Balke K., Wedler E., Peters S., Weitzenegger U., Wedler H., Balke K., Wedler E., Peters S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Abents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Frankz P.F.;

T. "Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. Columbia;
STRAIN=CV. Ammelem J., Chiapello H., Rouze P., Caboche M., Hofte H.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.,
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the LAE family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. Columbia;
Berthomieu P., Guerrier D., Giraudat J.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
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E -> D (IN REF. 4).
2026FC2852B7A2038 CRC64;
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PROSITE; PS00939; RIBOSOMAL_L1E; 1.
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Best Local Similarity 85./*
6, Conservative
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                                               SOLITIMENT DE REPRESENTANT DE
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01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 60S ribosomal protein L4 (L1).

88444KB

RPL4 OR RPL1.

407 AA.

STANDARD;

RL4 DROME P09180;

RESULT 29 RL4_DROME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. Bergeron; TISSUE=Mesocarp;
Mbeguie-A-Mbeguie D., Fils-Lycaon B.R.;
Molecular cloning and nucleotide sequence of a 60S ribosomal protein
L1 from apricot (Prunus armeniaca cv. Bergeron).";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prunus armeniaca (Apricot).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                    STRAIN=Oregon-R; MEDLINE=89098414; PubMed=2492096; Rafti F., Garziani F.; Rafti F., Gargiulo G., Manzi A., Malva C., Graziani F.; Rafti F., Harbosomal protein cDNA of D. melanogaster homologous storthe L1 ribosomal protein gene of X. laevis."; Nucleic Acids Res. 17:456-456(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                              "Isolation and structural analysis of a ribosomal protein gene in
                                                                                                                                                                                                                                          SEQUENCE OF 63-186 FROM N.A.
MEDLINE=88262486; PubMed=3133637;
Rafti F., Gargiulo G., Manzi A., Malva C., Grossi G., Andone S.,
Graziani F.;
                                                                                                                                                                                                                                                                                                                                                                  -!-SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
 Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 33; DB 1; Length 407; 85.7%; Pred. No. 1e+02; 1; Indels :ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 117 K -> R (IN REF. 2).
407 AA; 45755 MW; F35D7898770B043C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60S ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002136; Ribosomal L4/L1E.
Pfan; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL L1E; 1.
                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 16:4915-4926(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X13382; CAA31759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , X06881; CAA29998.1; -. S02209; RSFFL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0003279; RpL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 PRVRGGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=36596;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              D.melanogaster.
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RL4A_ARATH
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                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
Salanoubat M., LemcKe K., Rieger M., Perez-Alonso M., Obermaier B.,
Salanoubat M., LemcKe K., Rieger M., Perez-Alonso M., Obermaier B.,
Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Wincher P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Banger F.,
Wizedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60S Tibosomal protein L4-2 (Lil).
RPL4B OR AT3G09630 OR FIFB.22.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
            Loreni F., Ruberti I., Bozzoni I., Pierandrei-Amaldi P., Amaldi F.; "Nucleotide sequence of the Li ribosomal protein gene of Xenopus laevis: remarkable sequence homology among introns."; EMBO J. 4:3483-3488(1985).
                                                                                                            Amaldi F., Beccari E., Bozzoni I., Luo Z.-X., Pierandrei-Amaldi
"Nucleotide sequences of cloned cDNA fragments specific for six
                                                                                                                                                      Gene 17:311-316(1982).
-!-SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 396; 85.7%; Pred. No. 98; 1; Indels iive 0; Mismatches 1; Indels
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L -> P (IN REF. 2).
HAI -> MH (IN REF. 2).
R -> K (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002136; Ribosomal L4/L1B. Pfam; PF00573; Ribosomal L4; 1. PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                            Xenopus laevis ribosomal proteins.";
                                                                                         SEQUENCE OF 286-396 FROM N.A. MEDLINE=82262793; PubMed=7049839;
         MEDLINE=86135987; PubMed=3841512;
                                                                                                                                                                                                                                                                                                                                                                                                                                   321 321 L
337 339 HA
382 382 R
396 AA; 44906 MW;
                                                                                                                                                                                                                                                                                                          EMBL; X05217; CAA28844.1; -. EMBL; V01438; CAA24699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                      PIR; B24579; R5XL1B.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _TaxID=3702;
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Q9SF40;
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CONFLICT
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RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., RA Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E., Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mewes H.-W., RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., RA Roney T., Rizzo M., Walls A., Utterback T., Fujii C.Y., Shea T.P., RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., RA Rooney T., Rizzo M., Maiti R., Utterback T., Fujii C.Y., Shea T.P., RA Rooney T., Nierman W.C., Salzberg S.L., White O., Venter J.C., RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C., RA Fraser C.M., Matsumoto M., Matsuno A., Muraki A., Kishida Y., Ra Sasamoto S., Kimura T., Ideaawa K., Kawashima K., Kishida Y., Ra Nakayama S., Nakazaki N., Shinpo S., Takeuni C., Wada T., Ra Matanabe A., Yamada M., Yasuda M., Tabata S., Muraki A., Shinpo S., Takeuchi C., Wada T., Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CY. Columbia;
WEDLINE=21016721; PubMed=11130714; Kotani H., Kato T., Asamizu E.,
Tabata S., Kaneko T., Nakamura Y., Hosouchi T., Kawashima K.,
Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T.,
Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
Babter B., Cordum H., Cordes M., Courtney I., Courtney W., Dante M.,
Belter E., Cordum H., Cordes M., Courtney I., Latreille P.,
Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 AA; 44702 MW; A56AFA6CEAF291F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60S ribosomal protein L4-1 (L1). RPL4A OR RPL4 OR RPL1 OR AT5G02870 OR F9G14_180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P49691; Q9LXZ8;
01-FFB-1996 (Rel. 33, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; ACO16661; AAF23293.1; -.
Interpro; IPR002136; Ribosomal_L4/L1E.
Pfam; PF00573; Ribosomal_L4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress)
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Ribosomal protein.
SEQUENCE 406 AA: 44702 MW. BECARE
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Best Local Similarity 85./*
Best Local Similarity 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:820-822(2000).
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                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                        STRAIN=Bristol N2;
Fulton K., Wohldmann P.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.3%; Score 33; DB 1; Length 386; 85.7%; Pred. No. 96; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.3%; Score 33; DB 1; Length 345; 85.7%; Pred. No. 85;
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 AA; 38659 MW; C798B9DB0CED60AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FRB-1996 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF000196; AAC24253.1; -.
PIR; T34031; T34031.
WORMPEP; B0041.4; CE07669.
INTERPIC; IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00573; Ribosomal_L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U30495; AAA74021.1; -. PIR; T12048; T12048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 PRVRGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPL4 OR RPL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; T12048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RL4 URECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=86135987; PubMed=3841512;
Loreni F., Ruberti I., Bozzoni I., Pierandrei-Amaldi P., Amaldi F.;
"Nucleotide sequence of the L1 ribosomal protein gene of Xenopus
laevis: remarkable sequence homology among introns.";
EMBO J. 4:3483-3488 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPL4B OR RPL1B.
Renopus lavis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 33; DB 1, Length 396; 85.7%; Pred. No. 98; 1; Indels rative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA29796).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 246 P -> L (IN REF. 1; CAA29796).
392 392 P -> A (IN REF. 1; CAA29796).
396 AA; 44935 MW; 2DA0FB693A1186BC CRC64;
                                                                                                                                   P084<u>7</u>59; Q91843;
01-AUG-1988 (Rel. 08, Last sequence update)
10-AUG-1988 (Rel. 08, Last sequence update)
6-CCT-2001 (Rel. 40, Last annotation update)
60S ribosomal protein L4A (L1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L4B (L1B) (Fragment).
                                                                                                                     396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002136; Ribosomal_L4/L1E. Pfam; PF00573; Ribosomal_L4; 1.
                                                                                                                                                                                                                           RPL4A OR RPL1A.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00939; RIBOSOMAL_LLE; 1. Ribosomal protein. P. 246 CONFLICT 246 P -> L CONFLICT 392 P -> A
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05216; CAA28843.1; -. EMBL; X06552; CAA29796.1; -. PIR; A24579; R5XL1A.
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                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 PRVRGGG 87
                               76 PRVRGGG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRVTGGG 8
2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                     RL4A XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                    RL4A_XENLA
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-CZECH II; TISSUE-Mammary gland;

XI ALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XI ALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XI Diatchenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,

XI Diatchenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,

XI Diatchenko L., McEwan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XI Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XI Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XI Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Halon D.K., Wuzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

XI Hakesley T.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

XI Blakesley R.W., Touchman J.W., Grene E.D., Dickson M.C.,

XI Blakesley R.W., Tucchman J.W., Grene E.D., Dickson M.C.,

XI Blakesley R.W., Tucchman J.W., Grene E.D., Dickson M.C.,

XI Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XI Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

XI Generation and initial analysis of more than 15,000 full-length

XI Froc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89174988; PubMed=2494194; Saunders S., Jalkanen M., O'Farrell S., Bernfield M.; Molecular cloning of syndecan, an integral membrane proteoglycan."; J. Cell Biol. 108:1547-1556(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/c; TISSUB=Liver;
MEDLINE=93266605; PubMed=8496192;
Hinkes M.T., Goldberger O., Neumann P., Kokenyeji R., Bernfield M.;
"Organization and promoter activity of the mouse syndecan-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Romaris M., Coomans C., Ceulemans H., Bruystens A.-M., Vekemans S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular polymorphism of the syndecans. Identification of a hypoglycanated murine syndecan-1 splice variant.";
J. Biol. Chem. 274:18667-18674(1999).
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vihinen T., Auvinen P., Alanen-Kurki L., Jalkanen M.; "Structural organization and genomic sequence of mouse syndecan-1
                                                                                                                                                   SDC1 MOUSE STANDARD;
P18878, Q62278; O9WVD2;
P1.NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SDC1 OR SYND1 OR SYND1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 268:17261-17269(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99303636; PubMed=10373479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93352511; PubMed=8349612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=NMRI; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Mammary gland;
MEDLINE=89174988; Publ
                                       240 PRTTGGAA 247
                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David G.
                                                                                                                              SDC1_MOUSE
                                                                                                           RESULT 22
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O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

N-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

CLINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

CLEAVAGE OF ECTODOMAIN (POTENTIAL).

Missing (in isoform 2).
                -i. FUNCTION: Cell surface proteoglycan that bears both heparan sulfate and chondroitin sulfate and that links the cytoskeleton to the interstitial matrix.
-i., SUBCELLULAR LOCAL MATRIX.
-i., ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pROSITE; PS00964, SYNDECAN; 1. Proteoglycan; Heparan sulfate; Transmembrane; Glycoprotein; Signal; Alternative splicing. POTENTIAL. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                Note=Minor isoform;
-!- SIMILARITY: Belongs to the syndecan proteoglycan family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 AA; 32904 MW; 283FEC396FF40FCE CRC64;
                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
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Last annotation update)
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0; Mismatches
                                                                                                                                                                                                                                                                                          IsoId=P18828-2; Sequence=VSP_007542;
                                                                                                                                                                                        Name=1;
IsoId=P18828-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNDECAN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTIG=VSP
J. Biol. Chem. 268:11440-11448(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003585; Neurexin-like.
InterPro; IPR001050; Syndecan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X15487; CAA33514.1; -. EMBL, Z52532, CAA80254.1; -. EMBL, AF134897; AAA42345.1; -. EMBL, BC10560; AAH10560.1; -. EMBL, L11565; AAA40159.1; -. PIR; S06619; S0661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01034; Syndecan; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60S ribosomal protein L4. RPL-4 OR B0041.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                                                                          Note=Major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00294; 4.1m; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 PRVEGGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRVTGGG 8
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RL4_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ignatovich O., Cooper M., Kulesza H.M., Beggs J.D.; "Cloning and characterisation of the gene encoding the ribosomal protein S5 (also known as rp14, S2, YS8) of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-92184799; PubMed-1544921;
Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
"NH2-terminal acetylation of ribosomal proteins of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !- SIMILARITY: Belongs to the S7P family of ribosomal proteins
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                      62.3%; Score 33; DB 1; Length 223; 85.7%; Pred. No. 55; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
ROSE M., KOEtter. P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                         223 AA; 25257 MW; F87541F6CEC26D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
RPSS OR YUR123W OR J2045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 23:4616-4619(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD, SG003884; RPS5.
InterPro; IPR006235; Ribosomal S7.
InterPro; IPR005716; Ribosomal S7e/a.
Pfam; PF00177; Ribosomal S7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 267:5442-5445(1992).
                                                                                                                         PDB; 1KGO; 27-MAR-02.
InterPro; 1PR0013304; Lectin_C.
SMART; SW00034; CLECT; 1.
Hypothetical protein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000817; Ribosomal S7; 1.
TIGRFAMs; TIGR01028; S7_S5_E A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96103590; PubMed=8524651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X89368; CAA61550.1; -. EMBL; Z49623; CAA89654.1; -.
                                                            EMBL; V01555; CAA24860.1; -. PIR; F43042; QQBE26.
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GermOnline; 141956; -.
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PDB; 1K5X; 22-MAY-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 PRVRGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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RS5_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Du Z., Scheet P., Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity (By similarity).
-!- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolytic pathway.
-!- SUBUNIT: The proteasome is composed of at least 15 non identical subunits which form a highly ordered ring-shaped structure (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sumilarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMILARITY: Belongs to peptidase family T1A.
                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                         .
0
PROSITE; PS00052; RIBOSOMAL_S7; 1.
Ribosomal protein; Acetylation; Phosphorylation; 3D-structure.
                                                                                                                               62.3%; Score 33; DB 1; Length 224; 77.8%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00227; proteasome; 1. —
PROSITE; PS00388; PROTEASOME A; 1.
Proteasome; Hydrolase; Protease; Threcnine protease.
SEQUENCE 260 AA; 28311 MW; DSEEFFSE480F8F70 CRC64;
                                                   1 1 ACETYLATION.
20 20 T -> E (IN REF. 3).
224 AA; 24907 MW; A1354B6766981417 CRC64;
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62.3%; Score 33; DB
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF036694; AAB88344.1; -.
PIR; T32525; T32525.
HSSP; P40302; IRYP.
MEROPS; T01.976; -.
MormPep; CD4.6; CE16954.
InterPro; IPR001353; Pept T1 subA.
InterPro; IPR001353; Peptidase T1.
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                 145 TTRVGGGGA 153
                                                                                                                                                                                                           1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha 6).
PAS-6 OR CD4.6.
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044156;
                                                                       CONFLICT
                                     INIT MET
MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98295987; PubMed=954230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Bacham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Geoger K., Skelton S., Squares S., Squares R., Seeger V., Skelton S., Squares S., Squares R., Shalton J.B., Taylor K., Whitehead S., Barrell B.G.; Burlet B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
SIMILARITY: COAT PROTEINS FROM CARMOVIRUSES (CARMY, MNSV, TCV), DIANTHOVIRUSES (RCNMV), SOBEMOVIRUSES (MCMV, SBMV), TOMBUSVIRUSES (AMCV, CNV, CYRSV, AND TBSV), AND TNV ARE RELATED IN THEIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN, INTERACTION WITH RNA. DOMAIN, VIRION SHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 380;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical Perfamily protein Rv2892C/MT2959/MD2916C.
RV2892C OR MTCY274.23C OR MB2916C.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793CB6B05CEC6669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROJECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                  HSSP, P11795; ZTBV.
InterPro; IPR008975; Viral_cap_coat.
InterPro; IPR00037; Viral_coat.
Pfam; PF00729; Viral_coat. 1.
PRINTS; PR0023; ICOSAHEDRAL.
PROSITE; PS00555; ICOSAH_VIR_COAT_S; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN,
DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=M.tuberculosis; STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 AA; 40878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.2%;
50.0%;
                                                                                                                                                                                                                                            EMBL; M25270; AAA42904.1; -.
PIR; JA0131; VCVGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 TPSISGGGTI 327
                                                                                                                                                                                                                                                                                                                                                                                                                               254
380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Coat protein.
DOMAIN
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                                                                    REGION
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                 PERCIES—M. Dovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pror M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Parvor M., Duthoy S., Grondin S., Mayes R., Keating L., Wheeler P.R., Parris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.",
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-: SIMILARITY: Belongs to the mycobacterial PPE family.
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIINE=04270667; PubMed=6087149;
MEDIINE=04270667; PubMed=6087149;
MEDIINE=04270667; PubMed=6087149;
Gibson T.G., Farrell P.G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 408;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist; Rv2892c; -.
InterPro; IPR000030; Microbac_PPE.
InterPro; IPR00031; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSWEM 56 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3E3D1F20D7827199 CRC64;
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Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-UUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical BZLF2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.2%; Scor.
60.0%; Pred. No. ec,
7. 2; Mismatches
                                                                                                           J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE007119; AAK47285.1; -. EMBL; BX248344; CAD96603.1; -. PIR; G70925; G70925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 AA; 41469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z74024; CAA98377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 SPSVAGGGAV 301
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                                                                                         laboratory strains.";
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YZL2 EBV
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                                                                                                                        Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Bardero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chectuani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Brian K.-D., Reihl H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Jones L. M., Kaerst U., Kreft J., Kunn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nemmel B., Rose M., Schlueter T., Simose N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Science 294:849-852[2011].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01099; HYETHIZKNASE.
TIGREAMs; TIGR00694; thim; 1.
Thiamine biosynthesis; Transferase; Kinase; ATP-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: ATP + 4-methyl-5-(2-hydroxyethyl)-thiazole ADP + 4-methyl-5-(2-phosphoethyl)-thiazole.
-1- COFACTOR: Binds 2 magnesium ions per subunit (By similarity).
-1- PATHWAY: Thiamine blosynthesis.
-1- PATHWAY: Thiamine blosynthesis.
-1- SIMILARITY: Belongs to the Thz kinase family.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase) (TH kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.2%; Score 34; DB 1; Length 269; 55.6%; Pred. No. 43;
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MAGNESIUM 1 (BY SIMILARITY).
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                Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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InterPro; IPR000417; Hyethyz_kinase.
Pfam; PF02110; HK; 1.
                                                                           SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 123 M
269 AA; 28166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL596164; CAC95574.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ListiList; LIN00341; -.
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  Listeria innocua.
                                    NCBI_TaxID=1642;
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    MEDLINE=21537279; PubMed=11679669;
Glager P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glager P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glager P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chaxraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Domenn E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Gautier L., Goebel W., Gamez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreif J., Kuhn M., Kunst F., Kurapkat G.,
Andueno E., Mattournam A., Mata Vicente J., Ng E., Nedjari H.,
Andueno E., Mattournam A., Mata Vicente J., Ng E., Nedjari H.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Comparative genomics of Listeria species W.,
Comparative genomics of Listeria species W.,
Science 294:849-852(2001).
C. -- CATALYTIC ACTIVITY: ATP + 4-methyl-5-(2-hydroxyethyl)-thiazole G. -- PATHWAY: Thiamine Diosynthesis.
C. -- PATHWAY: Thiamine Diosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rochon D.M., Tremaine J.H.;
"Complete nuclectide sequence of the cucumber necrosis virus genome.";
Virology 169:251-259(1989)
-:- SUBUNIT: THE VIRUS COAT IS COMPOSED OF 180 COPIES OF THE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumber necrosis virus (CNV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiamine biosynthesis; Transferase; Kinase; ATP-binding; Magnesium; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.2%; Score 34; DB 1; Length 269; 55.6%; Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGNESIUM 1 (BY SIMILARITY)
MAGNESIUM 1 (BY SIMILARITY)
74A32D672176242C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the Thz kinase family.
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01-APR-1990 (Rel. 14, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00228; -; 1.
InterPro; IPR000417; Hyethyz_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=89204896; PubMed=2705296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AL591974; CAD00843.1; -. PIR; AE1114; AE1114.
ListiList; LMO00316; -.
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269 AA; 28052 MW;
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STRAIN=EGD-e / Serovar 1/2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE
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PROTEIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mech. Dev. 76:197-201 (1998).

Liberthouse Transcription repressor capable of inhibiting the transcription repressor capable of inhibiting the transcription capability of B47. May play a role in regulating transcription capability of E47. May play a role in regulating antigen-dependent B-cell differentiation.

Subunt: Efficient DNA binding requires dimerization with another bench protein. Binds DNA as a homodimer or a heterodimer. Forms a heterodimer with E12/E47.

SUBCELLULAR LOCATION: Nuclear.

COUNTIONS REPECTIOTY: Expressed in lymphoid tissues, B-cell lines and activated B cells.

COUNTION: Ref.1 sequence differs from that shown due to a frameshift in position 189.
MEDLINE=22388257; PubMed=12477932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B. Altschul S.F., Jeeperg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B. Batchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

A villalon D.K., Muzzy D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rahakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robb L., Hartley L., Wang C.-C., Harvey R.P., Begley C.G.; "Musculin: a murine basic helix-loop-helix transcription factor gene expressed in embryonic skeletal muscle."; Mech. Dev. 76:197-201 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50808; HLH; 1.
Transcription regulation; Repressor; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 603628; -. Groudleus; TAS. GO; GO:0005634; C:nucleus; TAS. GO; GO:0003714; F:transcription co-repressor activity; TAS. GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0006366; F:transcription from Pol II promoter; TAS. InterPro; IPR001092; HIM_basic. Pfam; PF00010; HIM; 1. SWART; SM00363; HIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF060154; AAC15071.1; ALT_FRAME.
EMBL, BC006313; AAH06313.1; -.
EMBL; AF087036; AAC69870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLU-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=98440284; PubMed=9767165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 6-206 FROM N.A.
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85
91
91
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160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T04902; -
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Germonine; 141109; -.

SGD, S0003029; DUOL.

GO; GO:0000778; C:condensed nuclear chromosome kinetochore; IPI.

GO; GO:000519; C:spindle; IPI.

GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.

GO; GO:0000210; P:structural constituent of cytoskeleton; IPI.

GO; GO:0000071; P:mitotic spindle assembly (sensu Saccharomyces); IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97377993; PubMed=9234674; Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes.";
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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0
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01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 27.5 kDa protein in PYCl-UBC2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase) (TH kinase).
THIM OR LIN0341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.2%; Score 34; DB 1; Length 247; 75.0%; Pred. No. 40; 1; Mismatches 1; Indels
                                             64.2%; Score 34; DB 1; Length 206; 85.7%; Pred. No. 33;
                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 247 AA; 27473 MW; 787F8AF869E3C978 CRC64;
DSD -> ASA (IN REF. 1).
21066E02553EB80C CRC64;
                                                                   Pred. No. 33;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
189 191 Di
206 AA; 22067 MW;
                                                                                                                                                                                                                                                                               (Rel. 34, Created)
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                                                                                   6; Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keast 13:861-869(1997).
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                                                                                                                                                       75 PRVAGGG 81
                                                                                                                      2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                               01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIM LISIN
Q92EW7;
                                                                                                                                                                                                                                                                                             01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                            YGG1 YEAST
P53168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
CONFLICT
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Heim M.A., Jakoby M., Werber M., Martin C., Weisshaar B., Bailey P.C.;
"The basic helix-loop-helix transcription factor family in plants: a
genome-wide study of protein structure and functional diversity.";
Mol. Biol. Bvol. 20:735-747(2003).
-!- FUNCTION: Transcription factor acting positively in the
                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
Schoenbohm C., Weisshaar B.;
Coverview of the bHLM transcription factor gene family in Arabidopsis
thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.; K.;
Hayashizaki Y., Shinozaki R.; Carninci B., Kawai J.,
Marabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni M., Tepperman J.M., Quail P.H.;
"Binding of phytochrome B to its nuclear signalling partner PIF3 is reversibly induced by light.";
Nature 400:781-784(1999).
                                                                                                                                             SEQUENCE FROM N.A.
STRAINS-C. Columbia.
STRAINS-V. YI H., Shin B., Song P.-S., Choi G.,
"Identification and characterization of three phytochrome-associated
      MEDLINE=99059501; PubMed=9845368;
Ni M., Tepperman J.M., Quail P.H.;
"PIF3, a phytochrome-interacting factor necessary for normal
photoinduced signal transduction, is a novel basic helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martinez-Garcia J.F., Hug E., Quail P.H.; "Direct targeting of light signals to a promoter element-bound transcription factor.";
                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99394605; PubMed=10466729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20259742; PubMed=10797009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 288:859-863(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana.";
Nature 408:816-820(2000).
                                                                                                     Cell 95:657-667(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                              proteins.
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                                    To the G box (5'-CACGTG-3').

Subuntry: Homodimer (Probable). Can form a heterodimer with REP1.

Phytochrome B binds specifically to DNA-bound PIF3, but only upon red light induced conversion to the Pfr form (PfrB). Reconversion to Pr form causes rapid dissociation.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

SIMPLARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
phytochrome signaling pathway. Activates transcription by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99252901; PubMed=9584154; Massari M.E., Rivera R.R., Voland J.R., Quong M.W., Breit T.M., van Dongen J.J.M., de Smit O., Murre C.! ""Characterization of ABF-1, a novel basic helix-loop-helix transcription factor expressed in activated B lymphocytes."; Mol. Cell. Biol. 18:3130-3139(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 35; DB 1; Length 524; 85.7%; Pred. No. 55; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, 186226; H66228.
HS$P, P25312; 1HLO.
TRANSPAC; T04492; -
InterPro; IFR01092; HLH basic.
Pfam; PF00010; HLH; 1.
PROSTIE; PS0808; HLH; 1.
PROSTIE; PS0808; HLH; 1.
Nuclear protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
E -> D (IN REF. 2).
S -> L (IN REF. 2).
1044AC01D598DE7C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSC_HUMAN STANDARD; PRT; 206 AA. 060682; 075946; 09BRB7; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2003 (Rel. 42, Last annotation update) Musculin (Activated B-cell factor-1) (ABF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF100166; AAC95156.1; ---
EMBL, AF088280; AAC9771.1; ---
EMBL, AF251693; AAL55715.1; ---
EMBL, AC003970; AAC33213.1; ---
EMBL, AX117255; BAC41930.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524 AA; 56990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytochrome signaling pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 85.7%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393
358
428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSC OR ABF1.
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TISSUE=Muscle;

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-!- SIMILARITY: Contains 1 fibronectin type III domain.

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C STRAIN-CSTBL/61; IISSUB-Embryonic stem cells;

XX Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arawau T., Hara A., Fukunishi X., Konno H., Adachi J., Fukuda S.,

A Arawawa T., Hara A., Fukunishi X., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Jashui K., Golobori T., Bono H., Kankawa T., Saito R.,

XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Kadola K., Matsuda H.A., Ashburner M., Baldarelli R., Barib G.,

XA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,

A Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Wyanhaw Boris M., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wyashisaki Y.,

A Wyashisaki Y.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhitching N., Manna J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).

-!- FUNCTION: Receptor for thymic stromal lymphopoietin (TSLP). Forms a functional complex with TSLP and IL/TR which is capable of stimulating cell proliferation through activation of STAT3 and STAT5. Also activates JAK2. Implicated in the development of the hematopoietic system.
-!- SUBCELIGIAR LOCATION: Type I membrane protein (isoform 1 and isoform 3). Secreted (isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q8CII9-2; Sequence=VSP_008788, VSP_008789;
                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing, Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q8CII9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2; Synonyms=Soluble CRLM-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 234-359 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIFF3 ARATH STANDARD; PRT; 524 AA.

(206536, Q9SBC5;
(28-FSB-2003 (Rel. 41, Last sequence update)
(28-FSB-2003 (Rel. 43, Last annotation update)
(28-FSB-2004 (Rel. 43, Last annotation update)
(39-FSB-2004 (Rel. 43, Last annotation update)
(30-FSB-2004 (Rel. 44, Last annotation update)
(30-FSB-2004 (Rel. 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ne, Glycoprotein, Alternative splicing.
POTENTIAL.
CYTOKINE RECEPTOR-LIKE FACTOR 2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> AGDPCAAHLPPL (in isoform 3).
/FTId=VSP 008790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 35; DB 1; Length 359; 77.8%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 15 A -> T (IN REF. 1).
51 51 G -> S (IN REF. 4 AND 5).
87 87 A -> G (IN REF. 4).
179 179 A -> V (IN REF. 1 AND 3).
309 309 P -> T (IN REF. 1 AND 3).
359 AA, 37761 MW, F9C52LC5484AC9DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (In isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> G (in isoform 2).
/FTId=VSP 008788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM0060; FN3; 1.
PROSITE; PS01355; HEMATOPO REC S_F1; FALSE NEG.
Receptor; Signal; Transmembrane; Glycoprotein; <sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSXWS motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                               EMBL; AB013945; BAA92684.1; -. EMBL; AB03133; BAA92159.1; -. EMBL; AF232936; AAF81676.1; -.
                                                                                                                                                                                                                                                                                                     EMBL, AF201963, AAF82189.1; -. EMBL, BC023788, AAH23788.1; -. EMBL, AK010291; BAB26827.1; -.
                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1889506; TBlpr.
InterPro; IPR003961; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
201
262
68
53
122
217
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0008285; P.negative regulation of cell proliferation; TAS. GO; GO:0045749; P:negative regulation of S phase of mitotic c. .; NAS. Growth arrest; GPI-anchor; Signal; Glycoprotein; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94173926; PubMed=8127893;

del Sal G., Collavin L., Ruaro M.E., Edomi P., Saccone S., Valle G.D.,
Schnetder C.;
Structure, function, and chromosome mapping of the
Structure, function, and chromosome of the murine gas1 gene.";
Proc. Natl. Acad. Sci. U.S.A. 91:1848-1852(1994).
-!- FUNCTION: Specific growth arrest protein involved in growth
suppression. Blocks entry to S phase. Prevents cycling of
normal and transformed cells.
-:- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0046658; C:extringic to plasma membrane, GPI-anchored; ISS. GO:0007050; P:cell cycle arrest; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROWTH-ARREST-SPECIFIC PROTEIN 1. REMOVED IN MATURE FORM (POTENTIAL) POLY-ALA.
                                                                                                                                                                                                                                                                          ö
                                                                                                                                            BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                          66.0%; Score 35; DB 1; Length 321; 77.8%; Pred. No. 34;
                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                           DC5E39EF3CCD114C CRC64;
             Pfam; PF01341; Glyco hydro 6; 1.

PRINTS; PR00733; GLHYDRASES.

PRODOM: PR003733; GLHYDRASES.

PROSITE; PS00655; GLYCOSYL HYDROL F6 1; FALSE NEG.

PROSITE; PS00656; GLYCOSYL HYDROL F6 2; 1.

CELlulose degradation; Hydrolase; Glycosidase; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Growth-arrest-specific protein 1 precursor (GAS-1).
                                                                                                                            ENDOGLUCANASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             345 AA
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
nterPro; IPR001524; Glyco_hydro_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                           33694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L13698; AAA72368.1; -.
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:4165; GAS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
345
345
                                                                                                                                            110
149
295
                                                                                                                                                                                                                                                                                                                                           274 TPTRTGGGA 282
                                                                                                                                                                                                                                                                                                              1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                              321 AA;
                                                                                                                                                                                                                                                           Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139185; -.
                                                                                                                                             110
149
295
112
                                                                                                                                                                                                                                                                                                                                                                                                                        GAS1_HUMAN
P54826;
                                                                                                                                             ACT SITE
ACT SITE
                                                                                                                                                                              ACT_SITE
DISULPID
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                               Query Match
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                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                 Matcheв
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QBCII9, Q9CRJ6; Q9JIB7; Q9JJH8; Q9JMD5;
QBCII9, Q9CRJ6; Q9JIB7; Q9JJH8; Q9JMD5;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cytokine receptor-like factor 2 precursor (Type I cytokine receptor delta 1) (Cytokine receptor-like molecule-2) (CRLM-2) (Thymic stromal lymphopoietin protein receptor) (TSLPR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of a novel type I cytokine receptor similar to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymphocytes;
MEDLINE=20197866; PubMed=10733486;
Rujio K., Nosaka T., Kojima T., Kawashima T., Yahata T.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Yamamoto K., Nishimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CS7BL/6; TISSUE=Lymphocytes;
MEDLINE=20432254; PubMed=109704
MEDLINE=20432254; PubMed=109704
Bark L.S., Martin U., Garka K., Gliniak B., Di Santo J.P., Muller W.,
Largaespada D.A., Copeland N.G., Jenkins N.A., Farr A.G.,
Ziegler S.F., Morrisesy P.J., Paxton R., Sims J.E.;
"Cloning of the murine thymic stromal lymphopoietin (TSLP) receptor.
Formation Of a functional heteromeric complex requires interleukin 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and characterization of CRLM-2, a novel type I cytokine receptor preferentially expressed in hematopoietic cells."; Biochem. Biophys. Res. Commun. 272:224-229(2000).
                                                                                                                                                                                                                                                                   Gaps
                                                                                  GPI-anchor amidated serine (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=21177258; PubMed=10881176;
MEDLINE=21177258; PubMed=10881176;
Bandey A., Ozaki K., Baumann H., Levin S.D., Puel A., Farr A.G.,
Ziegler S.F., Leonard W.J., Lodish H.F.;
"Cloning of a receptor subunit required for signaling by thymic
                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20329232; PubMed-10872831;
Hiroyama T., Iwama A., Morita Y., Nakamura Y., Shibuya A.,
Nakauchi H.;
                                                                                                                                                                                                    DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING
                                                                                                           117 N-LINKED (GLCNAC. . .) (PC
35721 MW; 2AAD50F1D3632F9D CRC64;
                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                      Pred. No. 36;
                                                                                                                                                                                                       Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                            POLY-GLY.
                                                            POLY-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1). STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Exp. Med. 192:659-670(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Immunol. 1:59-64(2000).
                                                                                                                                                                                                          66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 common gamma chain.";
Blood 95:2204-2211(2000).
                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphopoietin.
288
322
341
318
                                                                                                                                                                                                                                                                                                                                                                                           148 PRTSGGGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
285
319
337
318
117
345 AA;
                                                                                                                                                                                                                                                                                                                                  2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitamura T.;
                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stromal
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MEDLINE=22388257; PubMed=12477932;

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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression of branching enzyme II of maize endosperm in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
linkages in glycogen by scission of a 1,4-alpha-linked
oligosaccharide from growing alpha-1,4-glucan chains and the
subsequent attachment of the oligosac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                position.
CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-SUBUNIT: Monomer (By similarity).
-i-SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-i-SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11,4-alpha-glucan branching enzyme IIB, Chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme IIB) (Q-enzyme).
                                                                                                                                                                                                                                                                                  67.9%; Score 36; DB 1; Length 295; 66.7%; Pred. No. 20; ive 2; Mismatches 1; Indels
                                                                                           HAMAP; MF_00061; -; 1.
InterPro; IPR006204; GHMP_kinase.
InterPro; IR004424; ISPE.
Pfan; PF00288; GHMP_kinases; 1.
TIGRPAMS; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 248-271 AND 305-315.
STRAIN=cv. B73; TISSUE=Endosperm;
MEDLINE=95152344; PubMed=7849565;
Guan H.P., Baba T., Preiss J.;
                                                                                                                                                                                                                                              295 AA; 31085 MW; 18F318EEA2FAD384 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 58-65.
STRAIN=CV. W64A X 182E; TISSUB=Endosperm;
MEDLINE=94105320; PubMed=8278524;
Stsher D.K., Boyer C.D., Hannah L.C.;
"Starch branching enzyme II from maize endosperm.";
Plant Physiol. 102:1045-1046(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: Starch biosynthesis; third step.
                                                                                                                                                                                                                                ATP (POTENTIAL)
   modified and this statement is not removed.
                     entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 40:981-988(1994).
                                                                           EMBL; AE012186; AAM40186.1; -.
                                                                                                                                                                                                                                                                                                       66.78;
                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     242 TPŘLTGSGS 250
                                                                                                                                                                                                                                                                                                                                                               1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLGB MAIZE
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                    BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      008047;
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                            Malzeuri 19234; Alpha amyl cat.

R InterPro; IPR00604; Alpha amyl cat.

R InterPro; IPR00193; Glyco_hydro_l3N.

R Pfam; PF01028; Jabha-amylase; 1.

R Pfam; PF0292; isoamylase; 1.

R Glycogen biosynthesis; Starch biosynthesis; Transferase;

M Glycogyltransferase; Amyloplast; Chloroplast; Transit peptide.

TRANSIT 1 57 CHICKOPLAST (AMYLOPLAST).

TRANSIT 1 58 71 341 BY SIMILARITY.

TRANSITE 341 341 BY SIMILARITY.

TRANSITE 445 BY SIMILARITY.

TRANSITE 445 BY SIMILARITY.

TRANSITE 447 447 BY SIMILARITY.

FT ACT_SITE 445 BY SIMILARITY.

FT ACT_SITE 569 BY SIMILARITY.

FT ACT_SITE 569 S50 BY SIMILARITY.

FT ACT_SITE 570 S70 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.-!- SIMILARITY: Belongs to cellulase family B (family 6 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
8-EFBB-2003 (Rel. 41, Last annotation update)
Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)
(Cellulase I) (CMCASE I) (CELI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandez-Abalos J.M., Sanchez P., Coll-Fresno P.M., Villanueva J.R., Perez P., Santamaria R.I., "Cloning and nucleotide sequence of celA1, and endo-beta-1,4-glucanase-encoding gene from Streptomyces halstedii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 174:6368-6376(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 799;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                     0B440E0377BB087A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 28-33.
STRAIN=JM8 / CECT3310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=JM8 / CECT3310;
MEDLINE=93015685; PubMed=1400190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                       90517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          67.9%;
               EMBL; L08065; AAA18571.1;
PIR; T02981; T02981.
                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces halstedii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 PRLTGGG 23
                                                                                                                                                                                                                                                                                                                                                                         799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELLOBIOSE.
                                                      MaizeDB; 63943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydrolases)
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ACT_SITE
ACT_SITE
ACT_SITE
SCT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUN1_STRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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or send an email to license@isb-sib.ch).

EMBL; Z12157; CAA78145.1; -. HSSP; P26222; 1TML.

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us-10-697-055-7.rsp

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ISPE XANCP
Q8PC64;
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                    ISPE_XANCP
                                                                                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2002145; PubMed=12024217;

RA MEDLINE=22022145; PubMed=12024217;

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Guarotte G., Cannavan F., Cardollo M.C., Camargo L.B.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Fornighieri B.F., Franco M.C., Ferreira R.C.C., Ferro M.I.T.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Mortins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Mortins E.C., Machado M.A., Madeira A.M.B.N., Miyaki C.Y., Moon D.H.,

RA Mortins L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Sctubal J.C., Kitajima J.P.,

RA Nord Specificities, "...

RA Nord Specificities, "...
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol Kinase (EC 2.7.1.148) (CMK)
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol Kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATAINTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                        Score 36; DB 1; Length 254; Pred. No. 17; 0; Mismatches 1; Indels
                                                                                                                                                              7424D7D1339A5F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ispE family.
                                                                                                                                                                                                                                                                                                                                                      PRT; 295 AA.
                                                                                                                               PROTEIN GLIF.
                                                              EMBL; Abours...
PIR, 252581.
PIR, 252581.
ECGGene; EG1154; gltF.
Signal; Transmembrane; Complete proteome.
1 25 POTENTIAL.
 send an email to license@isb-sib.ch).
                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCC 13902 / XV 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                         EMBL; AE000401; AAC76246.1; -.
                                                                                                                                                        254 AA; 26351 MW;
                                                                                                                                                                                           67.9%;
                               EMBL; M74162; AAA23909.1; -.
                                                                                                                                                                             Query Match
Best Local Similarity 87.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 417:459-463(2002)
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                            EMBL; U18997; AAA58016.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPE OR IPK OR XAC0948.
                                                                                                                                                                                                                                                                                45 TPVVTGGG 52
                                                                                                                                                                                                                                                   1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bimilarity).
                                                                                                                                                                                                                                                                                                                                                        ISPE XANAC
                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                            RESULT 6
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Carburner From N.A.

STRAINSANCE 33913 / NCEPB 528;

RX MEDLINE=22022145; PubMed=12024217;

RA Gasjlva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Guaglo R.B., Monterior-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quagglo R.B., Monterior-Vitorello C.B., Van Sluys M.A., Ilmeida N.F.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cidarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Actia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katauyama A.M., Kishi L.T., Leite R.M. B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.R., Oliveira W.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., Ge Souza R.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R Thost Specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMK)
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).

    -!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 295;
                                                                                                                                                                                                                                                                            Pfan; PP00288; GHMP_kinases; 1.
TIGRRAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AA; 31057 MW; 9123D196F554A873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 36; DB 1; 66.7%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: Belongs to the ispE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris (pv. campestris).
        entities requires a license agreement
                                                                                                                                                             HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR004424; ISPE.
                                                                                                                       EMBL; AE011725; AAM35836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond (By similarity).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
-!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                    Gaps
            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "MOJECULAR CLONING and expression of rat prostasin.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses a trypsin-like cleavage specificity (By
                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                    ;
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN BER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                       Score 39; DB 1; Length 342;
Pred. No. 6.5;
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
Adachi M., Kitamura K., Miyoshi T., Tomita K.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
INTERCHAIN (BY SIMILARITY)
                                                                                                                                          0620DE88ED187D0F CRC64;
                                                                                                                                                                                                                                                                                                                                                  Q9ESB7; Q9ER01;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FB5-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      342 AA
                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase_SIA.
                                                                                                                                                                                                                                                                                                                                                                                                           Prostasin precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB017638; BAB20281.1; -. EMBL; AF202076; AAG32641.1; -.
                                                                                                                                              MW;
                                                                                                                                                                          73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00089; trypsin; 1.
                                                                                                                                              36729
                                                                                                                                                                                      Best_Local Similarity 75.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                             244
223
262
262
134
110
159
                                                                                                                                                                                                                                                                43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                  2 PRVTGGGA 9
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                          DISULFID
                                                                        ACT_SITE
ACT_SITE
ACT_SITE
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CARBOHYD
CARBOHYD
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DISULFID
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                                                                                                                                              SEQUENCE
                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- FUNCTION: INVOLVED IN INDUCTION OF THE SO-CALLED NTR ENZYMES IN
RESPONSE TO NITROGEN DEPRIVATION, AS WELL AS IN GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINS-XIZ / MGJ652.
STRAINS-XIZ / MGJ627.
STRAINS-3742617; PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , BIOSYNTHESIS. MAY MEDIATE THE GLUTAMATE-DEPENDENT REPRESSION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                     ACTIVATION PEPTIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%; Score 39; DB 1; Length 342; 75.0%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                      SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5ED1AF05D9213B98 CRC64;
                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (ECHARGE RELAY SYSTEM (ECHARGE
                                                                PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
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(Rel. 24, Last sequence update)
(Rel. 40, Last annotation update)
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2; Mismatches
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                                                                                                                        SIMILARITY.
                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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GLTF OR B3214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 PRITGGGS 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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37
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|ransmembrane
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01-DEC-1992
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ID GLTF ECOLI
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CARBOHYD
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                                                PROPER
                                                                                                                           ROPEP
                                                                                                                                                                              DOMAIN
                          SIGNAL
                                                                        CHAIN
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PROPEP
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                                                                                                                                                RESULT 3
PSS8 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87112940; PubMed=3027374; MEDLINE=87112940; PubMed=3027374; MEDLINE=87112940; PubMed=3027374; Medger B., Klages S., Walla B., Albrecht J.-C., Fleckenstein B., Tomlinson P., Barrell B.G.; Priminary structure and transcription of the genes coding for the two virion phosphoproteins pp65 and pp71 of human cytomegalovirus."; J. Virol. 61:446-453(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=64272751; PubMed=6087357;
MEDILINE=64272751; PubMed=6087357;
Mande H., Baak S.W., Riggs A.D., Clark B.R., Shively J.E., Zaia J. Bande H., Baak S.W., Riggs A.D., Clark B.R., Shively J.E., Zaia J. Rilodaing and physical mapping of a gene fragment coding for a 64-kilodalton major late antigen of human cytomegalovirus.";
kilodalton major late antigen of human cytomegalovirus.";
proc. Natl. Acad. Sci. U.S. A. 81.4965-4969(1984).
-!- FUNCTION: PORMS PART OF THE MATRIX OF THE HCMV VIRION.
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0
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                                                                                              100.0%; Score 53; DB 1; Length 551; 100.0%; Pred. No. 0.026;
                                                                                                                         0; Indels
                                                         462 462 PHOSPHORYLATION.
551 AA; 61638 MW; C56D11AEB01F3C23 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus (strain AD169).
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                            01-70N-1988 (Rel. 06, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                   65 kDa lower matrix phosphoprotein (PP65)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008649; Herpes UL82_83.
Pfam; PF05784; Herpes_UL82_83; 1.
Matrix protein; Phosphorylation.
EMBL; M67443; AAA45994.1; -.
InterPro; IPR008649; Herpes UL82_83.
Pfam; PF05744; Herpes UL82_83; 1.
MATXIX protein; Phosphorylation.
WOD_RES 462 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X17403; CAA35357.1; -.
EMBL, M15120; AAA45996.1; ALT_SEQ.
EMBL, K02531; AAA45983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90269039; PubMed=2161319;
                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                               407 TPRVTGGGAM 416
                                                                                                                                                        1 TPRVTGGGAM 10
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                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLETE GENOME.
                                                                                                                                                                                                                                                   PP65 HCMVA
P06725;
                                                                         SEQUENCE
                                                                                                    Query Match
                                                                                                                                                                                                                                        PP65_HCMVA
                                                                                                                               Matches
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                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20235202; PubMed=10770960; Use of the control of the control of the aniloride-sensitive epithelial sodium channel by the serine protesse mCAPI expressed in a mouse cortical collecting duct cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
-!- SIMILARITY: Belongs to peptidase family $1.
-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 339.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Am. Soc. Nephrol. 11:828-834 (2000).
-!- FUNCTION: Possesses a trypsin-like cleavage specificity (By similarity). Activates amiloride-sensitive sodium channels.
-!- SUBDNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Proetasin precursor (EC 3.4.21..) (Channel activating protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRSSB OR CAP1.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE (BY SIMILARITY). PROSTATIN LIGHT CHAIN. PROSTATIN HEAVY CHAIN. BY SIMILARITY.
                                                                                                              ..
                                                 100.0%; Score 53; DB 1; Length 561; 100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                              0; Indels
62898 MW; 37422EA149E88F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 342 AA.
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACHINEST PRODOBOOTS O'S SET LIYDBIN.
INTERPRO: IPRO01254; Peptidase S1.
INTERPRO: IPRO01314; Peptidase S1A.
Pfam.; PRO0109; LYYDBIN; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
SWART; SMO020; TRYP SPC; 1.
PROSITE; PSO0136; TRYPSIN DOM; 1.
PROSITE; PSO0135; TRYPSIN S1; 1.
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HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                       Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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prunus arme thermus sp. drosophila

DROME

RL4

P50878 rattus norv P36578 homo sapien Q8vca5 mus musculu Q9nrs4 homo sapien P09748 escherichia Q14757 homo sapien Q9nla6 drosophila P23944 rattus norv Q9ulc6 homo sapien Q8cq82 staphylococ P54741 streptomyce P54742 streptomyce Q81589 arabidopsis	P13126 deinococcus P55198 homo sapien P32790 saccharomyc Q9764 saccharomyc Q09734 trypanosoma Q09734 trypanosoma Q9714 trypanosoma Q97966 aeropyrum p Q00871 penaeus van P36178 penaeus van P36178 penaeus van P49307 thizobium m P39751 bacillus su P03185 epstein-bar P10664 saccharomyc P49626 saccharomyc P35679 schizosacch Q9784 schizosacch Q9785 prococcus P50316 pyrococcus P50316 pyrococcus	Q30255 pseudomonas Q03025 pseudomonas Q03025 pseudomonas Q19849 caenorhabdi pa4809 cryptococcu p44479 paemophilus Q35179 equus asinu P23388 r multiphos Q39747 porcine ade Q39747 porcine ade Q39747 porcine ade Q39747 porcine ade Q39748 aeropyrum p Q87125 vibrio para Q06114 mycobacteri poscoo mycobacteria myc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colinet D., Kummert J., Leppiyre P.;
"The nucleotide sequence and genome organization of the whitefly transmitted sweetpotato mild mottle virus: a close relationship with members of the family Potyviridae.";
Wirus Res. 53:187-196 (1988).
EMBL; Z73124; CAA97466.1; -.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sweet potato mild mottle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR INCLUSION PROTEIN A/B, COAT
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RECOFS; CU6.U01; -..

RECO; CO:0109028; C:viral capsid; IEA.

RECO; CO:0109028; F:ATP binding; IEA.

RECO; CO:01005026; F:ATP binding; IEA.

RECO; CO:01004197; F:ATP dependent helicase activity; IEA.

RECO; CO:01004197; F:Cysteine-type endopeptidase activity; IEA.

RECO; CO:01004197; F:Cysteine-type endopeptidase activity; IEA.

RECO; CO:0100507; F:Nucleic acid binding; IEA.

RECO; CO:01005079; F:RNA-directed RNA polymerase activity; IEA.

RECO; CO:01005198; F:RNA-directed RNA-directed RNA-directed
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Best Local Similarity 77.8%; Pred. No. 3.1e+03;
Matches 7; Conservative 1; Mismatches 1; Indels
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Best Local Similarity 77.8%; Pred. No. 1.4e+03; Matches 7; Conservative 0; Mismatches 2; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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CHAIN 1 743 HELPER COMPONENT.
CHAIN 744 863 HELPER COMPONENT.
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MEDLINE=98281520; PubMed=9620210;
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SMART; SM00490; HELICC; 1.
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RC STRAIN=C5PBL/6J; TISSUB=Embryonic stem cells;

RA MEDINE=2108566; PubMed=11217951;

RA Arakawa T., Shibata R., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Shibata R., Yoshino M., Adachi J., Fukuda S.,

RA Arakawa T., Izawa M., Nishi K., Konno H., Kasukawa T., Saito R.,

RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

RA Saito T., Buth C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Blake J., Boffelli D., Bolyunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Sato K., Scheombach C., Sakamoto N.,

RA Sato K., Scheombach C., Sakamoto N.,

RA Bashizaki M., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.,

RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Thymic stromal-derived lymphopoietin, receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AA; 13321 MW; BD387D755A8D9DF6 CRC64;
                                                                                                                                      126 AA
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                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AKO10291; BAB26827.1; -.
MGD; MGI:1889506; T8lpr.
                                                                                                                                            PRELIMINARY;
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3224 PRVTGFGAL 3232
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A Pattery T., Bayese C., Martens J., Chablain P., Parsons Y.N.,
A Pattery T., Bayese C., Martens J., Chablain P., Parsons Y.N.,
A Winstanley C., Cordwell S., Cornelis P.,
I Identification of the two undescribed ferrippoverdine receptors from seudomonas aerudinosa.";
Submitted (AUG-2020) to the EMBL/GenBank/DDBJ databases.
EMBL; AF537095; AAN62913.1;
CG) GO:0004872; Fireceptor activity; IEA.
GO; GO:0004872; Fireceptor activity; IEA.
GO; GO:0005215; Firenaport: IEA.
RO; GO:0005815; Firenaport: IEA.
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                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 823;
         67.9%; Score 36; DB 2; Length 808; 75.0%; Pred. No. 7.3e+02;
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Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                                     1; Indels
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-dependent protease ATP-binding subunit.
CLPB OR BLR1404.
                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   aeruginosa pyoverdine systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 143:35-43 (1997).
Query Match
Best Local Similarity 75.04
- - - - 6; Conservative
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                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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SEQUENCE FROM N.A.
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Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new CDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
BNBL, AB002373; BAA20830.2; -.
HSSP; Q61259; 1ABO.
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STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                               "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005940; BAC46669.1; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003754; F:peptidaes activity; IEA.
InterPro; IPR001959; AAA ATPRASe centr.
InterPro; IPR00170; Chaprnin_clpA/B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%; Score 36; DB 16; Length 879; 75.0%; Pred. No. 7.9e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1540 AA; 163853 MW; 5CC4D2C8FE77083B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0F935D239D7A3867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JRN-1998 (TrEMBLrel. 05, Created)
01-JRN-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA0375 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00004; AAA; 1. PFam; PF00004; AAA; 1. PRam; PF02861; Clp N; 2. PROTEASEA.
PROSITE; PF00870; CLPAB_1; 1. PROSITE; PF00871; CLPAB_2; 1. ATP-DIPP PROSITE; PF00871; CLPAB_2; 1. ATP-DIPP Proteases; Complete proteome. SEQUENCE 879 AA; 96621 MW; 0F935D239D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
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InterPro; IPR001452; SH3.
Pfam; PF02759; RUN; 1.
Pfam; PF00018; SH3; 1.
Probom; PD000066; SH3; 1.
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Best Local Similarity 75.v.
Fre 6; Conservative
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SMART; SM00326; SH3; 1.
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67.9%; Score 36; DB 4; Length 1540;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                      Gaps
       Makasa S.B.;

"Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";

Submitted (APR.2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ459318; CAD30642.1;

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0019079; P:RINA-directed RNA polymerase activity; IEA.

InterPro; IPR001592; Poty_coat.

InterPro; IPR007094; RNA_pol_PSvir.

Ffm.; PF00767; Poty_coat.
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                                                                                                                                                                                           67.9%; Score 36; DB 12; Length 501; 77.8%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                    i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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                                                                                                                                        227 501 COAT PROTEIN.
1 226 NUCLEAR INCLUSION B.
501 AA; 57263 MW; DOCE93F71AD0B91A CRC64;
                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Lipoate-protein ligase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 392:353-358(1998).

EMBL; AE000748; AAC07512.1; -.

PIR, C70441; C70441.

GO; GO:0016874; F:11gase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

GO; GO:0006464; P:protein modification; IEA.

InterPro; IPR004143; BPL LipA_LipB.

InterPro; IPR003704; CO dh/CoA synth.

Pfam; PF03099; BPL LipA_LipB.

Pfam; PF03552; CO_dh; 1.
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                                                                                                                                                                                                       Local Similarity 77.6 tes 7; Conservative
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                                                                                                                                                                                                                                                                         269 PRVTGFGAL 277
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134 RITGGGAI 141
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Best Local Similarity
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Aquifex aeolicus.
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081387
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067557
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STRAINECV. 173;

A Kim K.-N., Figher D.K., Gao M., Guiltinan M.J.;

Myolecular cloning and characterization of the amylose-extender gene encoding starch branching enzyme IIb in maize.";

"Molecular cloning and characterization of the amylose-extender gene encoding starch branching enzyme IIb in maize.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

B MRBL, AF072725; AAC33764.1; -.

R MRBL, AF072725; AAC33764.1; -.

R PIR; T01663; T01663.

CO; GO:0005507; F:copper ion binding; IEA.

CO; GO:0005507; F:copper ion binding; IEA.

CO; GO:0005489; F:electron transporter activity, hydrolyzing O-glycosyl ...; IEA.

CO; GO:0005837; F:hydrolase activity, hydrolyzing O-glycosyl ...; IEA.

CO; GO:0005489; F:electron transport; IEA.

CO; GO:0005489; F:electron transport; IEA.

CO; GO:0005418; P:electron transport; IEA.

R InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR004193; Glyco_hydro_13N.

InterPro; IPR007110; Ig-11Ke.

DR Ffam; PF00128; alpha-amylase; 1.

PFam; PF00128; alpha-amylase; 1.

PFam; PF00128; losamylase.).

R ROSITE; PS00196; COPPER BJUE; 1.

R ROSITE; PS00196; COPPER BJUE; 1.

R ROSITE; PS00196; COPPER BJUE; 1.

R ROSITE; PS00196; COPPER BJUE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                    Zea mays (Maize).
Warayota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Pfam; PF00593; TonB dep Rec; 1.
SEQUENCE 808 AA; 89414 MW; 4C7972A4D310E25C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Starch branching enzyme IIb.
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EMBL; AF$40992; AA017439.1; --
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005812; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
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                                                                                                                                                                                                                    Sweet potato mild mottle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                               Mukasa S.B.; "Analysis of the 3' terminal genomic region of sweet potato mild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mukasa S.B.;
"Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459315; CAD30639.1; --
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
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                    67.9%; Score 36; DB 12; Length 501; 77.8%; Pred. No. 4.5e+02; tive 1; Mismatches 1; Indels
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Submitted (Apr.-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459314; CAD30638.1; -
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:001079; P:viral genome replication; IEA.
InterPro; IPR001592; Poty coat.
InterPro; IPR0017094; RNA pol PSvir.
Pfam. PF00767; Poty_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 36; DB 12; Length 501; 77.8%; Pred. No. 4.5e+02; Live 1; Mismatches 1; Indels
501 AA; 57173 MW; 89DD08B244DBEC1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 226 NUCLEAR INCLUSION B.
501 AA; 57182 MW; FO6CD1D0061D3DB1 CRC64;
                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
                                                                                                                                              501 AA.
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                  Query Match
Best Local Similarity 77.8'
Matches 7; Conservative
                                                                                                                                            PRELIMINARY;
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Matches 7; Conservative
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                                                                                     269 PRVIGEGAL 277
                                                                2 PRVTGGGAM 10
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                                                                                                                                                                                                                                                     NCBI_TaxID=41459;
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                                                                                                                                                                                                                                              DOMOVITUS.
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SEQUENCE
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Q8B327
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Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ453016; CAD30640.1;
-
GO; GO:0013968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
InterPro; IPR01592; Poty.coat.
InterPro; IPR001592; RNA-dol-PSvir.
Pfam; PF00767; Poty.coat.
INTERPROSE IPR001592; RNA-DOL-PSVIR.
INTERPROSE IPR001592; RNA-DOL-PSVIR.
INTERPROSE IPR001592; RNA-DOL-PSVIR.
INTERPROSE IPR001592; RNA-DOL-PSVIR.
                                                                                                                                                                                        Score 36; DB 12; Length 501;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%; Score 36; DB 12; Length 501; 77.8%; Pred. No. 4.5e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                         1; Indels
                                                                                                                             1 226 NUCLEAR INCLUSION B.
501 AA; 57371 MW; D2C1967FEIEF5A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 1 226 NUCLEAR INCLUSION B. SEQUENCE 501 AA; 57204 MW; FF524F496A865F92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
GO; GO:0019079; P:viral genome replication; IEA. InterPro; IPR001592; Poty_coat. InterPro; IPR007094; RNA_pol_PSvir. Pfam; PF00767; Poty_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             501 AA
                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA
                                                                                                             COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sweet potato mild mottle virus.
                                                                                                                                                                                        67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.00,
                                                                                                                                                                                                              Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coat protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                           501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501
                                                                                                                                                                                                                                                                                                                      269 PRVTGFGAL 277
                                                                                                                                                                                                                                                                              2 PRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=41459;
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                                                                                          1
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RUK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pomovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ipomovirus
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                             Q8B325
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                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                               RESULT 41
Q8B325
                                                                                                                                                                                                                                    Matches
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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Ollver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.9%; Score 36; DB 16; Length 388; 75.0%; Pred. No. 3.5e+02; Live 2; Mismatches 0; Indels
                                                                                            Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Bentley S.D., Barrell B.G., Rajandream M.A.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                         67.9%; Score 36; DB 10; Length 38 75.0%; Pred. No. 3.5e+02; ative 1; Mismatches 1; Indels
                          383 AA; 40697 MW; D0336CA0423584CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliver K., Harris D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR04143; BPL LipA LipB.
Pfam; PF03099; BPL LipA LipB.
Hypothetical protein; Complete proteome.
SEQUENCE 388 AA; 41814 MW; 9AAIDE930DF6FC4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein SCO6423.
SCO6423 OR SCIA6.12C.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 AA.
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Nature 417:141-147(2002).
EMBL; AL939127; CAA18910.1; -.
PIR; T28693; T28693.
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Best Local Similarity 75.0۹
است 6; Conservative
                                                           Query Match
Best Local Similarity 75.v.
Fee 67 Conservative
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                                                                                                                                                                                                                       1 TPRVTGGG
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Gramene; Q9ARP7;
SEQUENCE 383 A
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069817
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Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mukasa S.B.;

Mukasa S.B.;

Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ459312; CAD30636.1;

EMBL; AJ459312; CAD30636.1;

EMBL; AJ459312; PRNA-directed RNA polymerase activity; IEA.

GO; GO:0019079; P:RNA-directed RNA polymerase activity; IEA.

InterPro; IPR001592; Poty_coat.

InterPro; IPR007094; RNA_pol_PSvir.

Pfam:

Pfam
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459313; CAD30637.1; -.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:019079; P:viral genome replication; IEA.
InterPro; IPR001592; Poty_coat.
InterPro; IPR00767; RNA_Pol_Psvir.
PRO; FRO; FOYCO31; Poty_cat: 1.
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Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 226 NUCLEAR INCLUSION B.
501 AA; 57249 MW; 77EF5647FB966A6C CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                             501 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sweet potato mild mottle virus.
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Best Local Similarity 77.00,
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01-MAR-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                        205 RISGGGAM 212
3 RVTGGGAM 10
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Probable lipoate protein ligase.
SNOP OR BL1217.
                                                                                     67.9%;
75.0%;
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OSJNBA0010K01.19.
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SEQUENCE
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Ylihonko K., Tuikkanen J., Jussila S., Cong L., Mantsala P.;
"A gene cluster involved in nogalamycin biosynthesis from Streptomyces nogalater: sequence analysis and complementation of early-blocked mutations in the anthracycline pathway.";
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                                  Loessner M.J., Inman R.B., Lauer P., Calendar R.; "Complete nucleotide sequence, molecular analysis and genome structure of bacteriophage Al18 of Listeria monocytogenes: implications for
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MEDLINE=96349102; PubMed=8760909;
Ylibonko K., Hakala J., Kunnari T., Mantsala P.;
Production of hybrid anthracycline antibiotics by heterologous expression of Streptomyces nogalater nogalamycin biosynthesis genes.";
Microbiology 142:1965-1972 (1996).
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MEDLINE=98007868; PubMed=9349712;
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Torkkell S., Yihonko K., Hakala J., Skurnik M., Mantsala P.;
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ24512; CAB59005.1; -.
PIR; T46683; T46683.
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03374; ANT; 1. _ . SEQUENCE 262 AA; 30217 MW; 11B66231BDB6F440 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004143; BPL_LipA_LipB.
PF03099; BPL_LipA_LipB; 1.
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                                                                                                                                                                                            Mol. Microbiol. 35:324-340(2000).

EMBL; AJ242593; CAB53832.1; -.

GO; GO:0003677; F:DNA binding; IEA.

InterPro; IRR005039; Anti_rep.
MEDLINE=20117992; PubMed=10652093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 87.5 es 7; Conservative
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Q9RIP7
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Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae; Oryza.
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MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F., Stabentonium reflects its ad
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Bifidobacteriaceae; Bifidobacterium.
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                                                        Score 36; DB 2; Length 354; Pred. No. 3.2e+02; 2; Mismatches 0; Indels
354 AA; 38074 MW; 4C7674E1F23741DD CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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EMBL, AE014148; AAN25024.1; -...
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004143; BPL Lipa Lipa.
PF03099; BPL Lipa Lipa.
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SEQUENCE FROM N.A.
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01-OCT-2003
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MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:226-531 (2003).
BMBL, AP005507, BA775291.;
Hypothetical protein; Complete proteome.
SEQUENCE 244 AA; 26824 MW; E953E6C988699ABD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                       MEDLINE=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptery; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 16; Length 244; Pred. No. 2.2e+02; 0; Mismatches 3; Indels
                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
       Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 70.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 TPRPTGGAKM 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG11294 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                              metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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DD111D
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lauko P., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mshrefi A., RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shies R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Williams S.M., Woodage T.Y., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao X.H., Myers B.W., Rubin G.M., Venter J.C., RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C., Ra Gience 287:2185-2195(2000).

C. -I -SUBCELLULAR LOCATION NUCLEAR (BY SIMILARITY).

REBL, AEO03444; ARA446405.1; -. DR Flybase, FBR0033069; Call294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDINES 177256; Loessner M. J. Wendlinger G., Scherer S.; Lucessner M.J. Wendlinger G., Scherer S.; Heterogeneous endolysins in Listeria monocytogenes bacteriophages: a "Heterogeneous endolysins in Listeria monocytogenes bacteriophages: a new class of enzymes and evidence for conserved holin genes within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:transcription factor activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008155; P:metabolism; IEA.
InterPro; IPR001356; Aldehyde_dehydr.
InterPro; IPR001356; Aldehyde_dehydr.
InterPro; IPR00136; Paired_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 261 AA; 28643 MW; 27A9BF152F372FF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0667; ALDEHYDE DEHYDR GLU; 1. PROSITE; PSO0027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Microbiol. 16:1231-1241(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lysis cassettes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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B97, cv. CI187-2, cv. CML254, cv. CML258, cv. D940Y, cv. 1205, cv. IDS28, cv. IL101, cv. KI21, cv. KI3, cv. M162W, cv. M017, cv. N28HT, cv. NC260, cv. NC348, cv. OH43, cv. PA91, cv. T232, cv. TX601, and cv.
                                                                                                                                                                                                                                                                                                                                                                                                     Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S. IV.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX235251; AAPD3728-1; -
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                                                                                                       MEDLINE=22247734; PubMed=12244216; Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S.; "Genetic diversity and selection in the maize starch pathway."; Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 36; DB 10; Length 139; 85.7%; Pred. No. 1.3e+02; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AA; 14579 MW; 7BC21F5F025F418D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY235279; AAP03756.1; -. GO, GO:005507; P:copper ion binding; IEA. GO; GO:005589; P:electron transporter activity; IEA. GO; GO:000518; P:electron transport; IEA. InterPro; IRR000923; BlueCu 1. PROSITE; PS00196; COPPER_BLÜE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Blr6432 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY235257, AAP03734.1; -- AY235258; AAP03735.1; -- AY235269; AAP03736.1; -- AY235260; AAP03737.1; -- AY235262, AAP03739.1; --
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EMBL; AY235275; AAP03752.1; -.
EMBL; AY235276; AAP03753.1; -.
EMBL; AY235277; AAP03754.1; -.
EMBL; AY235279; AAP03755.1; -.
EMBL; AY235279; AAP03755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AAP03730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY235255; AAP03732.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY235252; AAP03729.1; -.
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Best Local Similarity 85./۱
است 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PRVTGGG 8
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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           SO DER PRESENTATION OF THE PROPERTY OF THE PRO
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                                                                                                                  Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.,
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MEDLINE-21588047; PubMed=11731481;

A Huang J., Lih C.J., Pan K.H., Cohen S.N.;

Huang J., Lih C.J., Pan K.H., Cohen S.N.;

Tegulation of antibiotic biosynthetic pathways in Streptomyces

Tegulation of Intibiotic biosynthetic pathways in Streptomyces

Tegulation of Intibiotic biosynthetic pathways in Streptomyces

Golioo03824; Ficatalytic activity; IEA.

GO: GO:0003824; F:catalytic activity; IEA.

GO: GO:000444; P:protein modification; IEA.

InterPro; IPR004143; BPL_LipA_LipB.

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                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bardyrhiczbium japonicum USDA110.";
DNA Res. 9:189-197(2002)
EMBL; AP005958; BAC51697.1; -.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%; Score 36; DB 16; Length 181; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 36; DB 2; Length 222; 75.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         181 AA; 20587 MW; 73C8E7C8781DE6EF CRC64;
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Last annotation update)
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NCBI TaxID=100226;
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last anno
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01-00T-2002 (TrEMBLrel. 22, Last seq
01-00T-2003 (TrEMBLrel. 25, Last ann
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                                                          STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
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70 PRIIGGGA 77
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[1]
SEQUENCE FROM N.A.
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Length 139;
139 139 139 139 AM; 0D196F5F025F493B CRC64;
                                                                         67.9%; Score 36; DB 10; L
85.7%; Pred. No. 1.3e+02;
tive 1; Mismatches 0;
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                                                                                                                                        Conservative
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Matches 6; Conserv
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084JQ6;
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STRAIN=cv. PI566689;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY232419; AA092759.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000923; BlueCu I.
PROSITE; PS00196; COPPER_BLÜE; 1.
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoldeae; Andropogoneae; Zea.
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MEDLINE=22247134; PubMed=12244216;

Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S.;

"Genetic diversity and selection in the maize starch pathway.";

Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
                                                                                                                                                                                Zea mays (subsp. parviglumis) (Balsas teosinte).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MEDLINE-22247134; PubMed=12244216;

Mitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;

"Genetic diversity and selection in the maize starch pathway.";

Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                       Amylose extender 1 (Fragment). AE1.
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Les 6; Conservative
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STRAIN=CV. PI566691;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                      Zea mays (subsp. parviglumis) (Balsas teosinte).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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STRAIN=cv. PI566691;
MEDLINE=22247734 PubMed=12244216;
Whitt S.N. Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
Whete diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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85.7%; Pred. No. 1.3e+02;
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SEQUENCE FROM N.A.
STRAIN=CV. P1331785;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AX32417; AA092757.1;
GO, GO,000507; F:copper ion binding, IEA.
GO, GO.0005489; F:electron transporter activity; IEA.
GO, GO:0006118; P:electron transporter activity; IEA.
InterPro; IPR000923; BlueCu.1.
PROSTITE; PS001164; COPPER_BUUE; 1.
                                                                                                           STRAIN-cv. IC-3; White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.; White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY232416; AA092756.1; -...
GO, GO:0005489; F:clopter ion binding; IEA.

GO, GO:0005489; F:clectron transporter activity; IEA.

GO; GO:0006118; P:clectron transport; IEA.

InterPro; IPRO00923; BlueCu 1.

PROSITE; PSOUL9; COPER_BIŪE; 1.
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STRAIN=cv. PI331785;
MDELINE=22247734 PubMed=12244216;
White E.S., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
"Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962 (2002).
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.; "Genetic diversity and selection in the maize starch pathway."; proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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85.7%; Pred. No. 1.3e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             67.9%; Score 36; DB 10; Length 139; 85.7%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                          139 AA; 14494 MW; 7BD905F058AAF03D CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender 1 (Fragment).
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Best Local Similarity 85...
6; Conservative
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17 PRLTGGG 23
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Matches 6; Conserv
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17 PRLTGGG 23
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                                                                                          SEQUENCE FROM N.A.
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Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AX232415; AAO92755.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005608; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000923; BlueCu_1.
PROSITE; PS00196; COPPER_BLUE; 1.
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Eukaryota; Viridiplantae; Streptophyta; mbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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MEDLINE=22247734; PubMed=12244216;
WEDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
Whitt S.R., Wilson L.M., Tenaillon in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962 (2002).
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                                                        67.9%; Score 36; DB 10; Length 139;
85.7%; Pred. No. 1.3e+02;
ive 1; Mismatches 0; Indels
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                    139 AA; 14664 MW; 1E45805F0248DE83 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=22247734; PubMed=12244216;
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                                                  Query Match
Best Local Similarity 85./*
---- 6; Conservative
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17 PRLTGGG 23
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           MEDLINE=95207408; PubMed=7534933;
Liaine M.J., Metzler M.C., Zhong Y.P.;
Liaine M.J., Metzler M.C., Zhong Y.P.;
Liaine M.J., Metzler M.C., Zhong Y.P.;
"IS1237 a repetitive chromosomal element from gram-negative and gram-positive bacteria.";
If plasmid 32:270-279(1994).
R BMBL; X75973; GAA53586.1; --
R GO; GO:0004972; P:receptor activity; IEA.
R GO; GO:0004972; P:receptor activity; IEA.
R GO; GO:0006801; P:transporter activity; IEA.
R GO; GO:0006810; P:transporter activity; IEA.
R GO; GO:0006810; P:transporter activity; IEA.
R R GO; GO:000810; P:transporter activity; IEA.
R R GO; GO:000810; P:transporter activity; IEA.
R R GO; GO:000810; P:transporter activity; IEA.
R GO; GO:000810; P:transporter activity; IEA.
R GO; GO:000810; P:transporter activity; IEA.
R R GO; GO:000810; P:transporter activity; IEA.
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EMBL, AV235261; AAP03738.1; -in binding; IEA.

GO; GO:0005549; F:electron transporter activity; IEA.

GO; GO:0006118; P:electron transport; IEA.
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Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MEDLINE=22247734, PubMed=12244216;
Whitt S.N., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S.;
Whitt S.N., Wilson L.M., Tenaillon in the maize starch pathway.";
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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01-00N-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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PROSITE; PS00196; COPPER_BLUE; 1.
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17 PRLTGGG 23
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STRAIN=cv. F2;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY235264; AAP03741.1; -.
GO; GO:0005519; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006189; P:electron transport; IEA.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                               Zea mays subsp. mays (maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Mbitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-2224734; PubMed=12244216; Milt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.; Whit S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.; "Genetic diversity and selection in the maize starch pathway."; Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962 (2002).
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85.7%; Pred. No. 1.3e+02;
ive 1; Mismatches 0; Indels
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GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:000549; F:electron transporter activity; IEA.
GO; GO:000518; P:electron transport; IEA.
InterPro; IPR00923; BlueCu 1.
PROSITE; PS00196; COPPER BLUE; 1..
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender starch-branching enzyme (Fragment)
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender starch-branching enzyme (Fragment)
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                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Mat. Biotechnol. 21:256-531(2003).

EMBL; APO05041; BAC72891.1;

GO; GO:0009274; C:cell wall (sensu Bacteria); IEA.

GO; GO:0009274; C:cell wall (sensu Bacteria); IEA.

GO; GO:0009252; P:penicillin binding; IEA.

GO; GO:0009252; P:pepticallin binding; IEA.

InterPro; IPR001264; Glyco_trans 51.

InterPro; IPR001460; Transpeptdse.
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                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRALNE-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572949;
MEDLINE-21477403; PubMed=11572949;
Omutra S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
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NCBI_TaxID=33903;
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.8%; Score 37; DB 16; Length 748; 75.0%; Pred. No. 4.5e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
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MEDLINE=21477403; Pubmed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 AA; 78005 MW; 9073C631F670EEA1 CRC64;
                                                                                                                                                                                                                               STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
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Last annotation update)
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                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                   Streptomycineae; Streptomycetaceae; Streptomyces.
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01-JUN-2003 (TrEMBLrel. 24, Last seqn
01-JUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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Best Local Similarity 75.uv
Since 6; Conservative
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 Streptomyces avermitilis.
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SAV5477.
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huzar L., Hyman R.W., Rahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymk megaplasmid.";
Phroc. Natl. Acad. Sci. U.S.A., 98:9883-9888 [2001).
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                 Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
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Micrococcineae; Microbacteriaceae; Leifsonia.
NCBL_TaxID=1575;
[1]
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein RA0336.
RA0336 OR SMA0638.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Plasmid pSymA (megaplasmid 1).
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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                                                                                                                                                                                                                                                                     Score 36; DB 16; Length 54;
Pred. No. 50;
3; Mismatches 1; Indels
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Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 85 AA; 9300 MW; 8C966E072243521C CRC64;
                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 54 AA; 5884 MW; 7FE1DFB025140016 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ORF2 frame shift at position 226.
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                                                                                                      microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005043; BAC73189.1; -.
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                        67.9%;
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Best Local Similarity 60.0.
Best Local 6; Conservative
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28 SPYMTGGGAL 37
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69.8%; Score 37; DB 10; Length 379; 77.8%; Pred. No. 2.3e+02; ive 0; Mismatches 2; Indels

7; Conservative

2 PRVTGGGAM 10

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yeast one-hybrid system method.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY341856; AAQ20915.1; -
SEQUENCE 379 AA; 39956 WW; - B233AD060113C84D CRC64;
                                                                                                                                      Local Similarity
                                                                                                                Query Match
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Yao Q., Peng R., Xiong A.;
"Isolation of rice WRKY protein through W-box bait vector by modified
                                                  Gaps
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:PO688A04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.8%; Score 37; DB 10; Length 379; 77.8%; Pred. No. 2.3e+02; Live 0; Mismatches 2; Indels
Query Match

69.8%; Score 37; DB 16; Length 345;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone:P0006C01.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative DNA-binding protein homolog.
P0688R04.2 OR P0006C01.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 379 AA.
                                                                                                                                                                                                                                                           PRT; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002839; BAB19096.1;
EMBL; AP002744; BAB19075.1;
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Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                           192 PKLAGGGAM 200
                                                                                                  2 PRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                         Q9FE35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 AA; 70503 MW; 395D98388A3772DF CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Penicillin-binding protein, 1A family.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last seq 01-007-2003 (TrEMBLrel. 25, Last ann putative penicillin-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 TPMKRVTGGGA 586
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                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caulobacter crescentus.
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339 PAVAGGGAM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=155892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
SEQUENCE 653 AA
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Q9ABH5
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MEDLINE=2282794; PubMed=12910271;

MEDLINE=2282794; PubMed=12910271;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Cerdeno-Tarraga A.M., Colling M., Cronin A., Davis P., Doggett J.,

Cellingworth T., Colling M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Colling M., Cronin A., Davis P., Doggett J.,

Reltwell T., Goble A., Hamlin M., Hauser H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Chaparative analysis of Lie genome sequences of Bordetella pertussis,

Wat. Genet. 35:32-40 (2003).

Nat. Genet. 35:32-40 (2003).

Rell. Bridetella parapertusis and Bordetella bronchiseptica.";

Rell. Bridetella Parapertusis and Bordetella bronchiseptica.";

Rell. Bridetella Parapertusis and Bordetella bronchiseptica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                           Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 16; Length 25:
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
3 258 AA; 28296 MW; 2246BDF651E190AF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative lipoate-protein ligase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TOHama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271;
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EMBL; BX640414; CAE41593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%;
                                                                                                                                                                                 STRAIN=12822 / ATCC BAA-587;
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Best Local Similarity 87.5.
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 RVSGGGAM 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AA;
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=519;
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69.8%; Score 37; DB 16; 87.5%; Pred. No. 1.6e+02;

Best Local Similarity

Query Match

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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P., Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.; "The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus.";

Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                               MEDLINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
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                                                                                                                                                                                                                                          Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 16; Length 20:
Pred, No. 1.66+02;
 Indels
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                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
 0;
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EMBL; BX572101; CAE22321.1; -.
Hypothetical protein; Signal; Complete proteome.
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 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 345 AA; 38138 MW; 05F9948CD
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                                                                                                                                                                01-0CT-2003 (TrEMBirel. 25, Created) 01-0CT-2003 (TrEMBirel. 25, Last seq 01-0CT-2003 (TrEMBirel. 25, Last and Hypothetical protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=22709201; PubMed=12810954;
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(TrEMBLrel. 25,
(TrEMBLrel. 25,
7; Conservative
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Matches 6; Conservative
                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter hepaticus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                               ||:|||||
81 RVSGGGAM 88
                             3 RVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPRVTGGG 8
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Prochlorococcus.
NCBI_TaxID=74547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=32025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                   Q7V426;
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Matches
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kosema B., Lim J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Saku M., Schinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F1511.14.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                                                                                                                                   Gaps
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STRAIN-cv. Columbia;
Vysotekaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotekaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lid J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federapiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC F15I1 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                   ;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
F1511.14 protein (Putative DNA-binding protein) (Hypothetical
                                                                                                                                                                                      71.7%; Score 38; DB 11; Length 340; 85.7%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theologis A.; "Full Length cDNA of gene F1511.14 (GI:4587547)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Full Length cDNA of gene F1511.14 (GI:4587547).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                  PFam, PF00089; trypsin, 1.
PRINTS, RR00725; CHYMCTRYREIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HSE; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 340 AA; 36503 MW; 3C2540E9B3A81CBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
InterPro; IPR001314; Peptidase_SIA.
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                                                                                                                                                                      Query Match
Best Local Similarity Bo...
S. Conservative
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43 PRITGGG 49
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CSTRAINE-ERBSO / ATCC BAA-588;

WEDLINE-22827954; PubMed=12910271;

WEDLINE-22827954; PubMed=12, James K., Harris B., Quail M.A.,

Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Dagest J.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Reltwell T., Goble A., Hamlin N., Hauser H., Bornder D., Seeger K.,

Rabbinowitch E., Summers M., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; Squares S., Stevens K.,

Comparative analysis of the genome sequences of Bordetella pertussis,

RE Bordetella parapertussis and Bordetella bronchiseptica.";

ENEL, BKG4445; CALESS38331; -.
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Alcaligenaceae; Bordetella.
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                   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
                                                                                                                                                                                                                                                                      71.7%; Score 38; DB 10; Length 383; 87.5%; Pred. No. 1.5e+02; ative 0; Mismatches 1; Indels
                                                                  "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006577; AAD28778.1;
EMBL; AF360325; AAX26035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus)
                                                                                                                                           EMBL, AY056333; AAL07182.1; -.
EMBL; AY084772; AAM61340.1; -.
PIR, C96881; C96581.
G0; G0:0003677; F:DNA binding; IEA.
Hypotherical protein; DNA-binding.
SEQUENCE 383 AA; 41731 MW; D7AE4D93DAF2BIEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 AA; 28296 MW; 2246BDF651E190AF CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7W618;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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                                                                                                                                                                                                                                                                                            Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        62 TPSVTGGG 69
                                                                                                                                                                                                                                                                                                                                                    1 TPRVTGGG 8
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               SEQUENCE FROM N.A.
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Q7W618
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OVAIGO
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RESULT 4
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The Ago is a style of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of the following of the mouse transcriptome based on functional annotation of the following the mouse transcriptome based on functional annotation of the following transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of the following transcriptome based on function of the following transcriptome 
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
[2]
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS0134; TRYPSIN_HIS; 1.
SEQUENCE 255 AA; 27355 MW; 1P96A6EF2431FF73 CRC64;
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protease, serine, 8 (Prostasin).
PRSS8.
                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
     0.53;
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                               0; Mismatches
  Pred. No.
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100.08;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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                            10; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                        417 TPRVTGGGAM 426
                                                                                   1 TPRVTGGGAM 10
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43 PRITGGGS 50
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 10; Conser
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Q99L44
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Eye;

MEDINE=22354683; PubMed=12466851;

The FANTOM Consortium.

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of G0,770 full-length cDNAs.";

Nature 420:563-573(2002).

REBL, AKO76869; BAC37362.1; -.

REBL, AKO76869; BAC37362.1; -.

REDL, AKO7689; FISHARSTYPSIN activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

RO; GO:0006289; P:proteolygis and peptidolysis; IEA.

RO; GO:0004295; P:trypsin activity; IEA.
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SEQUENCE FROM N.A. STRAINSTRELUNG: STRAINSTREAUGHOUS G.W. Caughey G.H.; "Werghese G.M., Caughey G.H.; "Molecular cloning and characterization of mouse prostasin, a type I membrane-associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                "mouse serine protesse.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMIT PRODOS; LTYPSIN; 1.

PRINTS; PRO072; CHYMOTRYPSIN.

SMART; SM00020; TTYP_SPC; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

Hydrolase; Protesse; Serine protesse.

SEQUENCE 339 AA; 36216 MW; BC2DE88BC057AF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1928810; PrssB.
GO; GO:0004253; F:chymotrypsin activity; IEA.
GO; GO:0004225; F:cpptidase activity; IEA.
GO; GO:0004225; F:trypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001205; Peptidase_SI.
InterPro; IPR001254; Peptidase_SIA.
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                                                                                                                                                                                                                                                                                                                Kitamura K., Takefumi N., Kimio T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BC003851, AAH03851.1; -. EMBL, AR378086; AAL06320.1; -. EMBL, AR3780895; AAL06310.1; -. EMBL, AB038244; BAB82496.1; -.
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Q9akx4 legionella Q8nd25 homo sapien O18487 penaeus van O701379 bordetella Q701378 bordetella Q80136 bordetella Q701378 bordetella Q8014 streptiomyce Q81418 agrobacteri Q9x21 brucella su Q8x21 brucella su Q8x25 brucella su Q8x25 brucella su Q8x41 brucella su Q8xx4 ralstonia su Q8xx4 ralstonia su Q8xx4 ralstonia su Q8xx5 staphylococ Q80x18 streptococc Q80x1 streptococc Q97491 streptococc Q97491 streptococc Q97491 streptococc Q97491 streptococc Q97491 streptococc Q97491 streptococc Q9105 homo sapien Q8bury arabidopsis Q9545 pendomonas Q91445 pan rhadino Q9144 pan rhadino Q91444 pan rhadino Q914444 pan rhadino Q914444 pan rhadino Q9144	as ar
455 32 60.4 269 2 Q9AXX4 456 32 60.4 271 4 QBND25 459 32 60.4 271 16 Q7U379 459 32 60.4 271 16 Q7U379 450 32 60.4 271 16 Q7U379 460 32 60.4 271 16 Q7U379 60.4 271 16 Q7U379 60.4 272 2 G06950 60.4 294 2 Q08724 466 32 60.4 294 2 Q08724 66 32 60.4 294 2 Q08722 60.4 292 60.4 292 16 Q087X4 472 32 60.4 329 16 Q087X4 472 32 60.4 329 16 Q087X4 473 32 60.4 329 16 Q087X4 473 32 60.4 333 2 Q02631 477 32 60.4 333 2 Q02631 477 32 60.4 335 16 Q087X7 5 60.4 336 10 Q087X7 5 60.4 336 10 Q087X7 5 60.4 336 12 Q0184 5 60.4 364 12 Q0184 5 60.4 364 12 Q0184 5 60.4 369 12 Q0184 5 60.4 389 12 Q0184 5 60.4 390 17 Q0572 6 6	32 60.4 396 16 G7VGQ3 32 60.4 398 16 G9ZG78 32 60.4 403 16 G9ZG78 32 60.4 413 16 G9ZG78 32 60.4 417 16 G9ZG78 33 60.4 417 16 G9ZG78 34 MATCH 30 00.0 \$ SCORE 53; DB 12;
Q9fiv4 streptomyce Qgc504 mus musculu Qg76ff saccharomyc Q875w0 saccharomyc Q875w9 saccharomyc Q875w9 saccharomyc Q875w9 saccharomyc Q875w3 saccharomyc Qgaaxz caulobacter Q9axz caulobacter Q9axz caulobacter Q9axz drosophila Q7x196 oryza sativ Q7x0b8 mycobacteri Q700b8 mycobacteri Q700b8 mycobacteri Q9d46 drosophila Q9gv6d drosophila	089jg1 bradyrhizob 06622 aquifex aeo 066124 streptromyce 089209 caulobacter 099093 controllobacter 091017 mus musculu 089mb3 bradyrhizob 0804m3 toryza sativ 0814m3 toryza sativ 0814m3 toryza sativ 0814m3 toryza sativ 0814m3 toryza sativ 0816m3 arabidopsis 0817m3 arabidopsis 080729 xanthomonas 080729 xanthomonas 080729 xanthomonas 080729 xanthomonas 080729 xanthomonas 080729 xanthomonas 080729 torsophila 095m1 corymabacter 096m1 corymabacter 096m1 corymabacter 096m1 deinococcus 086m1 coryma sativ 096m1 drosophila 095m3 deinococcus 086m1 drosophila 095m3 toryma sativ 090m1 drosophila 096m4 thizobium m 08705 thermoplasm 09705 thermoplasm 09705 sulfolobus 098m30 pseudomonas

Q7u5p8 synechococc Q81431 plasmodium Q81si4 chlamydomon	O9pky9 chlamydia m	Q7wg54 bordetella	Q7w4m8 bordetella O59546 morganella	Q8ptl1 methanosarc	Obaino streptococc	Q8p2t1 streptococc	Q8k8s0 streptococc	Q8e3a5 streptococc	Oganis streptococc	Q93dbl streptococc	Q82az3 streptomyce	Q86683 drosophila 018545 caenorhabdi	0887g6 oryza sativ	Q8dn94 streptococc	Q7xna0 oryza sativ	20Apr. Crysa Barry Q9qw71 rattus sp.	OBjim1 brachydanio	Q7zvi2 brachydanio	Q91ev4 cydia pomon	Q8msv9 drosophila	O91179 streptomyce	29viiv, diosopiilid Q9sb64 arabidopsis	Q9yag6 aeropyrum p	Q7xkb8 oryza sativ O8eih2 shewanella	Q8fm34 corynebacte	09zxe7 bacteriopha	Q9q0az cnimpanzee Q9q094 chimpanzee	090273 chimpanzee	O9y2h5 cuimpanzee	Q910p1 streptomyce	Q)rqgı mus muscuru Q0iu42 dictyosteli	Q9v4u4 drosophila	Vall/2 drobopnila Q8xq42 ralstonia s	Q9lcu0 mycobacteri	O7vsm9 trypanosoma	Q9i7t7 drosophila	Qaswe/ micromonosp O7to67 rattus norv	093t34 haemophilus	Q9visl drosophila O869h2 lymnaea eta	Q9vap9 drosophila	083we8 micromonosp	Q8xqp2 ralstonia s	Q83wf0 micromonosp	Q7xtp8 oryza sativ	O18489 penaeus van	Q9q3p5 hepatitis c	Q8vma/ mizobium e Q93w83 arabidopsis	Q8s0z5 oryza sativ O8c3n8 mus musculu	Q8pfx7 xanthomonas	Q9mbis bacteriopha
33 62.3 409 16 Q7U5P8 33 62.3 411 5 Q81431 33 62.3 434 10 Q8LSI4	62.3 445 16	62.3 464 16	62.3 464 16	62.3 474 17	62.3 475 16	62.3 477 16	62.3 477 16	62.3 479 16	62.3 4.79 Ib	62.3 485 16	62.3 485 16	62.3 488 5	62.3 499 10	62.3 508 16	62.3 541 10	62.3 559 11	62.3 586 13	62.3 586 13	62.3 665 12	62.3 691 5	62.3 694 16	62.3 704 10	62.3 706 17	62.3 733 10 62.3 818 16	62.3 1003 16	62.3 1018 9	62.3 1023 15	62.3 1031 15	62.3 1048 4	62.3 1111 16	62.3 1218 5	62.3 1264 5	62.3 1371 16	62.3 1400 2	62.3 1522 5	62.3 1531 5	62.3 1683 11	62.3 1764	62.3 1843 5 62.3 2141 E	62.3 2977 5	62.3 3649 2	62.3 4106	62.3 4307 2	61.3 293 10	60.4 58	60.4 82 12	60.4 105 10	60.4 115	60.4 128 16 08	60.4 129 9
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33 62.3 219 4 Q9NFE2 33 62.3 223 16 Q7U471 33 62.3 225 16 Q92ST4	62.3 228 16	62.3 230 11	62.3 231 5	62.3 242 16	62.3 247 16	62.3 247 16	62.3 248 16	62.3 249 9	62.3 249 9	62.3 249 17	62.3 249 17	62.3 250 9	62.3 251 16	62.3 254 4	62.3 259 17	62.3 265 9	62.3 265 16	62.3 267 IO	62.3 291 5	62.3 292 10	62.3 296 5	62.3 310 5	62.3 310 5	62.3 311 10 62.3 314 10	62.3 314 16	62.3 321 2	62.3 329 10	62.3 333 16	62.3 337 16	62.3 337 16	62.3 339 10	62.3 339 16	62.3 346 5	62.3 347 10	62.3 356 2	62.3 356 16	62.3 363 10	62.3 366 2	62.3 375 10	62.3 375 13	62.3 376 16	62.3 381 10	62.3 385 13	62.3 396 13	62.3 401 13	62.3 402 16	62.3 404 16	62.3 405 4 62.3 406 10	62.3 406 17	62.3 407 10
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165 34 64.2 1065 10 07X539 165 34 64.2 1076 10 07X529 166 34 64.2 1076 10 07X129 167 34 64.2 1076 10 07X129 168 34 64.2 1081 10 07X129 169 34 64.2 1089 10 08S179 170 34 64.2 1109 10 094186 171 34 64.2 1109 10 094186 172 34 64.2 1110 10 08X27 173 34 64.2 1110 10 08X27 174 34 64.2 1110 10 08X27 175 34 64.2 1110 10 08X27 176 34 64.2 1110 10 08X27 177 34 64.2 1110 10 08X27 178 34 64.2 1110 10 08X27 189 34 64.2 1110 10 07X12 190 34 64.2 1110 10 07X12 191 34 64.2 1110 10 07X12 192 34 64.2 1110 10 07X12 193 34 64.2 1110 10 07X12 194 34 64.2 1110 10 07X12 195 34 64.2 1110 10 07X12 197 34 64.2 1110 10 07X12 198 34 64.2 1173 10 07X12 199 34 64.2 1173 10 07X12 190 34 64.2 1173 10 07X12 191 34 64.2 1173 10 07X12	33 62.3 174 18 33 62.3 177 17 33 62.3 177 17 33 62.3 180 16 33 62.3 191 10 33 62.3 191 10 33 62.3 201 4 33 62.3 201 8 33 62.3 201 8 33 62.3 201 8
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90 34 64.2 46 12 092572 91 34 64.2 126 0 Q7X545 92 34 64.2 252 16 09X035 94 34 64.2 263 16 09X035 95 34 64.2 263 16 09X045 96 34 64.2 263 16 09XRC5 97 34 64.2 263 16 09XRC5 100 34 64.2 273 9 10 09XRC4 101 34 64.2 278 10 04946 102 34 64.2 278 10 04946 103 34 64.2 278 10 04946 104 34 64.2 288 10 04946 105 34 64.2 288 10 04946 106 34 64.2 288 10 04946 107 34 64.2 288 10 04946 108 34 64.2 346 4 092774 109 34 64.2 346 4 092774 110 34 64.2 357 16 09XRC5 111 34 64.2 357 16 09XRC5 111 34 64.2 357 16 097KC4 112 34 64.2 357 16 097KC4 113 34 64.2 357 16 097KC4 114 64.2 379 12 099XC6 115 34 64.2 357 16 097KC4 115 34 64.2 357 16 097KC5 116 34 64.2 357 16 097KC5 117 34 64.2 357 16 097KC5 118 34 64.2 357 16 097KC5 119 34 64.2 357 16 097KC5 110 34 64.2 357 16 097KC5 111 34 64.2 554 10 077KC5 113 34 64.2 554 10 077KC5 113 34 64.2 659 10 077KC5 113 34 64.2 669 11 099WL5 113 34 64.2 669 11 077KC5 113 34 64.2 669 10 077KC5 114 34 64.2 666 11 077KC5 115 34 64.2 669 10 077KC5 114 64.2 935 10 077KC5 115 34 64.2 669 10 077KC5 117 34 64.2 669 10 077KC5 118 34 64.2 669 10 077KC5 118 34 64.2 669 10 077KC5 119 34 64.2 935 10 077KC5 140 34 64.2 935 10 077KC5 141 34 64.2 935 10 077KC5 142 34 64.2 935 10 077KC5 144 64.2 935 10 077KC5 145 64.2 935 10 077KC5 146 64.2 935 10 077KC5 147 64.2 935 10 077KC5	34 64.2 999 10 34 64.2 999 10 34 64.2 1099 10 34 64.2 1027 10 34 64.2 1037 10 34 64.2 1031 10

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098yg2 arabidopsis
07wig0 bordetella
07wsi8 bordetella
07vwi1 bordetella
07vy46 prochloroco
07vy46 helicobacte
09fe35 oryza sativ
09abh5 caulobacter
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APPLICANT:

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| Sublication No. US20030054421A1
| SABREAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
| CURRENT APPLICATION: NUMBER: US/10/102,806
| PRIOR APPLICATION: NUMBER: 09/25,298
| PRIOR PILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 846
| SOFTWARE: PATENTIN VUMBER: 60/124,270
| SEQ ID NO 730
| LENGTH: 288
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64.2%; Score 34; DB 9; Length 263;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
                    APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAXI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT PELLING DATE: 200-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQTEMARE: PATENTIN VET. 3.0
SEQTEMARE: PATENTIN VET. 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-4695
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-102-806-730
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86 RMSGGGAM 93
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US-10-102-806-730
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us-10-697-055-7.rapb

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                                                                                                                                                                             NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20030194721A1 3282941CD1 US-10-247-671-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION WOMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4633, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4695, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
ANDO, SEIKO
      PRIOR FILING DATE: 2001-09-19
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CCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
IKEDA, MASATO
OZAKI, AKIO
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4633
LENGTH: 260
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.73
Matches 6; Conservative
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                         NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 249-125
                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                    SEQ ID NO 173
LENGTH: 206
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APPLICANT:
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT PELING NUMBER: US,10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
RIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FaatSEQ for Windows Version 3.0
SEQ ID NO 262
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
GURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
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CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17800, Application US/10369493; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 173, Application US/10247671; Publication No. US20030194721A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0,
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SEQ ID NO 17800
LENGTH: 148
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                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-262
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ORGANISM: SPHINGOMONAS
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9 PKVPGGGA 16
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Best Local Similarity
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NESCONDERS OF A PARTICATION US/10219220

Sequence 71, Application US/10219220

Sequence 71, Application No. US20030082724A1

SEQUENCE INTERVALION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Geath and their use in the modification of plant development

TITLE OF INVENTION: death and their use in the modification of plant development

TITLE OF INVENTION UNMERS: US/10/219,220

CURRENT APPLICATION NUMBER: US/10/219,220

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 290

SEQ ID NOS: 290

SEQ ID NO 71

LENGTH: 86
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          Length 524;
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TITLE OF INVENTION: No. US20040005560A1el full length cDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
                                                       0; Indels
       Query Match
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2675, Application US/10108260A; Publication No. US20040005560A1; GENERAL INFORMATION:
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Matches 6; Conservative
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Matches 6; Conservative
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US-10-219-220-262
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Green, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6241
LENGTH: 522
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Best Local Similarity 70.0%; Pred. No. 6.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                    Query Match
Best Local Similarity 70.0%; Pred. No. 6.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels
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APPLICANT: Sato, Sae
APPLICANT: Sato, Sae
TITLE OF INVENTION: A UNIVERSAL LIGHT-SWITCHABLE GENE
TITLE OF INVENTION: A DECOMPTER SYSTEM
TITLE OF INVENTION: WIMBER: US/10/227,035
CURRENT APPLICATION NUMBER: US/10/227,035
CURRENT APPLICATION NUMBER: US/0/355,402
PRIOR APPLICATION NUMBER: US/0/355,402
PRIOR APPLICATION NUMBER: US/0/355,402
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ. ID NOS: 11
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6241, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Caenorhabditis elegans
                                               ; TVPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6240
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; ORGANISM: Arabidopsis thaliana
US-10-227-035-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Quail, Peter H. APPLICANT: Hug, Enamul
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LENGTH: 524
; SEQ ID NO 6240
; LENGTH: 522
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Gaps

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Gaps

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Sequence 6240, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF;

TITLE OF INVENTION: EXPRESSION OF MICROBIAL BROYER S.

TITLE OF INVENTION: UNMER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
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APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION'S Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION'S Gene Disruption Methodologies for Drug Target Discovery
TITLE APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
SUPTWARE: PATENT IN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 35; DB 14; Length 444; 66.7%; Pred. No. 5.4e+02; trive 0; Mismatches 3; Indels
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
LENGTH: 444
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Publication No. US20030180953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Candida albicans
US-10-032-585-7677
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Best Local Similarity 66.73
Matches 6; Conservative
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Matches 6; Conservative
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US-10-369-493-6240
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US-10-314-657-23

Sequence 23, Application US/10314657

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US2003017588A1

Sequence 23, Application No. US2003017588A1

Septicant: Hency 200-11

TITLE OF INVENTION: Synthases and Methods of Use

TITLE OF INVENTION: Synthases PCT/US02/08937

FRICK APPLICATION NUMBER: PCT/US02/08937

PRIOR APPLICATION NUMBER: PCT/US02-02-26

PRIOR APPLICATION NUMBER: US 60/278,935

PRIOR APPLICATION NUMBER: US 60/278,935

PRIOR FILING DATE: 2001-03-26

NUMBER OF EXQ ID NOS: 214

SOFTWARE: PatentIn version 3.2

SEQ ID NO 23

LENGTH: 432
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                      APPLICANT: "Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REPERSENGE: 21829/203 (EBC-003)
CURRENT APPLICATION NUMBER: 105/10/441,736
CURRENT FILING DATE: 2003-05-20
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-02
PRIOR PILING DATE: 1999-11-02
SOFTWARE: PALENTION NUMBER: 09/431,614
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PALENTION NUMBER: 09/431,614
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PALENTIN VOR: 2.1
SEQ ID NO 14
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; Sequence 7910, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OWURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, UUN
; APPLICANT: SHIRA, TADAYOSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIXUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptomyces atroolivaceus
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7°
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                   APPLICANT: Wei, Zhong-Min
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us-10-697-055-7.rapb

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169 rPTATGGGS 177
1 TPRVTGGGA 9
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Sequence 9, Application US/09835684

Batent No. US20020019337A1

GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Giu, Dewen
APPLICANT: Giu, Dewen
TITLE OF INVENTION: TRESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR TITLE OF INVENTION: DESICCATION
FILE REFERENCE: 21829/71

CURRENT FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/198,359
PRIOR FILING DATE: 2000-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wei, Zhong-Min
APPLICANT: DeRocher, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 21829/91
CURRENT APPLICATION NUMBER: US/09/880,371
CURRENT FILING DATE: 2001-06-13
PRIOR RPLICATION NUMBER: 60/211,585
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LIENGTH: 424
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                                                                                        Score 35; DB 9; Length 370;
Pred. No. 4.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09880371; Patent No. US20020059658A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas syringae
US-09-880-371-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Pseudomonas syringae
                                                                                              66.0%;
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SOFTWARE: PatentIn Ver. 2.1
                                                                                Ouery Match
Best Local Similarity 77.8-
Pest Local Similarity
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                                                                                                                                                                                                            344 PRGPGGGAM 352
                         ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-895-593-2
                                                                                                                                                                       2 PRVIGGGAM 10
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       LENGIH: 370
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US-10-010-390-9

| Sequence 9, Application US/10010390
| Sequence 9, Application US/10010390
| Publication No. US20330104979A1
| GENERAL INFORMATION:
| APPLICANT: Wel, Zhong-Min | APPLICANT: Usedo, Agustin | APPLICANT: Usedo, Agustin | TITLE OF INVENTION: REHONDS OF INHIBITING DESICCATION OF CUTTINGS REMOVED | TITLE OF INVENTION: REPRESENCE: 1282/111 | CURRENT APPLICATION NUMBER: US/10/010,390 | CURRENT FILING DATE: 2001-11-05 | PRIOR FILING DATE: 2001-11-05 | PRIOR FILING DATE: 2000-11-13 | NUMBER OF SEQ ID NOS: 14 | NUMBER OF SEQ ID NOS: 14 | SOFTWARE: Patentin Ver. 2.1
                                                   Sequence 14. Application US/09879248

Sequence 14. Application US/09879248

Patent No. US2002062500A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 2001-06-12

PRIOR APPLICATION NUMBER: 60/212,211

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 18

SEQTIMARE: Patentin Ver. 2.1

SEQUENCE: A PATENTIAL OF THE OFFICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.0%; Score 35; DB 9; Length 424; Best Local Similarity 66.7%; Pred. No. 5.2e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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US-10-441-736-14
Sequence 14, Application US/10441736
Publication No. US20040016029A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 rPTATGGGS 177
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Matches 6; Conserva
RESULT 34
US-09-879-248-14
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PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                    Query Match
Best Local Similarity 75.v.
Eest 6; Conservative
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                                                                                                                                                                                                                                                                               79 PRLAGGGA 86
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                                                                                              TYPE: PRT
ORGANISM: Human
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                                                                                 LENGIH: 361
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APPLICANT: Ozaki, Katsutoshi
APPLICANT: Baumann, Heinz
APPLICANT: Levin, Steven D.
APPLICANT: Ziegler, Steven F.
APPLICANT: Leonard, Warren F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Uses Thereof
TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Thymic Stromal
FILE REFERENCE: 00-514-E
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                                                                                                                                                                                                           Score 35; DB 9; Length 353; Pred. No. 4.3e+02; 0; Mismatches 2; Indels
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Publication No. US20030157118A1
GENERAL INFORMATION:
APPLICANT:
Coche, Thierry
APPLICANT:
Coche, Thierry
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Cassart, Jean-Pol
TITLE OF INVENTION: Tumour-Specific Animal Proteins
FILE REFERENCE: BC45300-1
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CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/215,658
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09895593; Patent No. US20020160949A1; GENERAL INFORMATION:
                                                                                                                                                                                                                 66.0%;
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APPLICANT: Ozaki, Katsutoshi
PRIOR FILING DATE: 2000-06-28
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Best Local Similarity 77.6-
Trace 7; Conservative
               NUMBER OF SEQ ID NOS: 16
SOTTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 353
TYPE: PRT
                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8'
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ORGANISM: Mus musculus
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; NAME/KEY: TRANSMEM
; LOCATION: (227)..(247)
US-09-895-593-3
                                                                                                                                     ; NAME/KEY: TRANSMEM
; LOCATION: (227)...(247)
US-09-895-943-3
                                                                                                                                                                                                                                                                                        2 PRVTGGGAM 10
                                                                                                         ORGANISM: Mus musculus
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                                                                                                                              FEATURE
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ORGANISM: Oryza sativa
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91 SPHVTGGG 98
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US-10-374-780A-1701
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LENGTH: 338
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US-09-895-943-3
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GRANEAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10058
LENGTH: 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.5%; Pred. No. 7.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: magnetite-containing magnetic coccus US-10-169-493-10058
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APPLICANT: OWNEA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKANA, UUN
APPLICANT: HORIKANA, HIROSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, MASHHIRA
APLICANT: HATORI, MASHHIRA
APLICANT: HATORI, MUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-02-09
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
                                                                                                  US-10-369-493-10058
; Sequence 10058, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9249, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
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                  22 VTGGGAM 28
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LENGTH: 330
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Sequence 170, Appliantion () (1914/190A)

Sequence 170, Appliantion () (1914/190A)

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sherman, Seadley K
APPLICANT: Sherman, Seadley Gia: Zhong
APPLICANT: Sherman, Seadley Gia: Zhong
APPLICANT: Sherman, Seadley Gia: Zhong
APPLICANT: Sherman, September 1, Unne
APPLICANT: Sherman, S
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RESULT 26

Gaps

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Sequence 20821

Sequence 20821

Sequence 20821

Publication No. US20030233675A1

SENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Blate, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

ITILE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES

ITILE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES

ITILE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20821

LENGTH: 600

WARNER NOTE OF THE CATTON OF THE CATTON OF THE CATTON NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

SEQ ID NO 20821

LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Goldan.
APPLICANT: Goldan.
TITLE OF INVENTION: EXFESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
GURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15324
LENGTH: 294
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Best Local Similarity 100.0%; Pred, No. 5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matchés 6; Conservative 2; Mismatches 1; Indels
  67.9%; Score 36; DB 15; Length 276; 66.7%; Pred. No. 2.3e+02; tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                   ; sequence 15324, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Xanthomonas campestris
Query Match
Best Local Similarity 66.7
- Local 6, Conservative
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Sequence 15690, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Good Yongon

APPLICANT: Good And And Barry

APPLICANT: Good And And Barry

APPLICANT: Good And And Barry

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROFERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

PRIOR FILING DATE: 2003-02-21

WUMBER OF SEQ ID NOS: 47374
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US,10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16082
LENGTH: 276
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                                                                                                                                                                                                                 67.9%; Score 36; DB 14; Length 244; 70.0%; Pred. No. 2e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 16082, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                        , ORGANISM: Streptomyces avermitilis
US-10-156-761-15056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Xanthomonas campestris US-10-369-493-15690
          PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 15056
LENGTH: 244
                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.0°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TPRLTGSGS 236
                                                                                                                                                                                                                                                                                                                                1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                 74 TPRPTGGAKM 83
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LENGTH: 276
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIRA, JUN
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: HATTORI, MCSHITUKI
APPLICANT: HATTORI, MCSHITUKI
APPLICANT: HATTORI, MCSHIRA
TITIE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-204089
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 15056, Application US/10156761; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 27829, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AL133476.4
                                                                    TYPE: PRT; CRGANISM: Streptomyces avermitilis US-10-156-761-13012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.0°
" Conservative 7;
                                                                                                                                         Query Match
Best Local Similarity 60.0.
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13012
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                                                                                                                                                                                                                                                  1 TPRVTGGGAM 10
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28 SPYMTGGGAL 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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US-10-156-761-15056
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US-10-029-386-27829
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LENGTH: 145
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Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                    Query Match

69.8%; Score 37; DB 14; Length 313;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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PUBLICATION NO. US20030119018A1

GENERAL INFORMATION:
APPLICANT: INEDA, HARUO
APPLICANT: INFITAMA, JUN
APPLICANT: SHIRA, HARUO
APPLICANT: SHIRA, TADAYOSHI
CURRENT HATYORI
APPLICANT: NOVEL POLYNUCLEOTIDES
FILE REFREENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30

PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HORITEWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SROUNBER OF SEQ ID NOS: 15109
SEQ ID NO 12713
LENGTH: 748
         NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12713, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; CRGANISM: Streptomyces avermitilis US-10-156-761-12713
                                                                                                                           ; ORGANISM: C. aurantiacus (22971932)
US-10-306-762-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 PRINGGGA 600
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                                                                                                               TYPE: PRT
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVID K.
TITLE OF INVENTION: HUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
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67.9%; Score 36; DB 14; Length 54; 60.0%; Pred. No. 45; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9 OTHER INFORMATION: EXPRESSED IN PLACEMYL, SIGNAL = 5.1 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7 OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 3.4 OTHER INFORMATION: SYMISSPROT HIT: 008788, EVALUE 1.60e+00
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APPLICANT: Glazebrock, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Kraps, Joel
APPLICANT: Moudhamer, Todd
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
FILE REFERENCE: 70029-NP
CURRENT FILING DATE: 2002-09-26
PRIOR PLLING DATE: 2002-09-26
PRIOR PLLING DATE: 2002-04-04
SPRIOR PLLING DATE: 2002-0
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73.6%; Score 39; DB 15; Length 665;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 39; DB 15; Length 342; 75.0%; Pred. No. 89;
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PRIOR APPLICATION NUMBER: 60/291,672
PRIOR FILING DATE: 2001-05-17
PRIOR PELING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 97
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 124, Application US/10259194A
Publication No. US20040010815A1
GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Grassemian, Rapid
APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus norvegicus
US-10-051-874-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0*
---- 6; Conservative
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27 TPRLSGGGTL 36
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:||||:
43 PRITGGGS 50
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US-10-259-194A-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Sequence 109, Application US/10306762

Publication No. US2003187220A1

GENERAL INFORMATION:
APPLICANT: Park, Frances
APPLICANT: Buchanan, Sean Grant
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
FILE REFERENCE: 52498-20011.00

CURRENT APPLICATION NUMBER: US/01/306,762

CURRENT FILING DATE: 2003-04-16

PRIOR PPLICATION NUMBER: US 60/334,132

PRIOR FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                        APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liana
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.7%; Score 38; DB 15; Length 383; 87.5%; Pred. No. 1.5e+02; Live 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: 09/837,944
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PELING DATE: 2001-04-18
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-22
PRIOR PELING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PELING DATE: 2001-11-19
PRIOR PELING DATE: 2001-11-19
PRIOR PELING DATE: 2001-12-11
PRIOR PELING DATE: 2002-06-14
PRIOR PELING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR PELING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
NUMBER OF SEQ ID NOS: 2906
                   APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline B
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                                                                                                                                                  Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
Reuber, T. Lynne
Keddie, James
Broun, Pierre E
                                                                                                Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5.
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US-10-374-780A-2854
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GENERAL INFORMATION:
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US-10-306-762-109
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LENGTH: 383
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APPLICANT: Stone, David J
APPLICANT: Burgees, Catherine E
APPLICANT: Burgees, Catherine E
TITLE OF INVENTION: USING THE SAME
FILE REPERENCE: 21402-02-245
CURRENT FILING DATE: 2001-02-14
PRIOR PELICATION NUMBER: 60/265,306
PRIOR PELICATION NUMBER: 60/265,469
PRIOR FILING DATE: 2001-02-16
PRIOR PELICATION NUMBER: 60/227,477
PRIOR FILING DATE: 2001-01-18
PRIOR PELICATION NUMBER: 60/296,777
PRIOR PILING DATE: 2001-03-16
PRIOR PELICATION NUMBER: 60/291,672
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
Taupher Jr, Kaymond J
Gerlach, Valerie
                                                                                                                                                                      Sequence 86, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                               APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
APPLICANT: Vernet, Corine AM
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MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
Pena, Carol EA
Tchernev, Velizar T
Zerhusen, Bryan D
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
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Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
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Ellerman, Karen
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43 PRITGGGS 50
2 PRVTGGGA 9
                                                                                                                              RESULT 11
US-10-051-874-86
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APPLICANT:
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APPLICANT: Stone, David J
APPLICANT: Burges Catherine E
APPLICANT: Burges Catherine E
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
                                                                                                                                                Gaps
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                                                                                                       Query Match
73.6%; Score 39; DB 15; Length 342;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR PILING DATE: 2001-01-18
PRIOR PELING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
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Herrman, John L
Peyman, John A
Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
Taupier Jr, Raymond J
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Publication No. US20040005557A1
GENERAL INPORMATION
APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
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Zerhusen, Bryan D
Millet, Isabelle
Miller, Charles E
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Spytek, Kimberly A
Boldog, Ferenc
Vernet, Corine AM
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Shimkets, Richard A
Pena, Carol EA
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Grosse, William M
Liu, Xiaohong
Ellerman, Karen
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MacDougall, John R
Malyankar, Uriel M
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Smithson, Glennda
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Stone, David J
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Shenoy, Suresh G
Casman, Stacie J
; SEQ ID NO 86
; LENGTH: 342
; TYPE: PRI
; ORGANISM: Rattus norvegicus
US-10-051-874-86
                                                                                                                                                                                                                     ||:||||:
43 PRITGGGS 50
                                                                                                                                                                                           2 PRVTGGGA 9
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APPLICANT:
APPLICANT:
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APPLICANT:
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SEQ ID NO 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.6%; Score 48; DB 14; Length 10; 100.0%; Pred. No. 0.083; tive 0; Mismatches 0; Indels
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US/09/692,170C
PRIOR FILING DATE: 2000-12.20
PRIOR FILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 1098-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-16
PRIOR PILING DATE: 1998-05-16
PRIOR PILING DATE: 1998-02-10
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
SEQ ID NOS: 44
SEQ ID NOS: 44
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LOCATION: (10)...(10)

OTHER INFORMATION: Xaa = L, F or M
US-10-405-231-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Padigaru, Muralidhara APPLICANT: Alsobrook II, John P APPLICANT: Colman, Steven D APPLICANT: Spytek, Kimberly A APPLICANT: Boldog, Perenc APPLICANT: Vernet, Corine AM
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Pena, Carol EA
Tchernev, Velizar T
Zerhusen, Bryan D
Millet, Isabelle
Miller, Charles E
Lepley, Denise M
Smithson, Glennda
Baumgartner, Jason C
Herrman, John L
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Gerlach, Valerie
Grosse, William M
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Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
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Malyankar, Uriel M
Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
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Kekuda, Ramesh
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Matches 9; Conserv
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APPLICANT:
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APPLICANT: Estiernan, Maren
APPLICANT: Stone, David Jark
TITLE OF INVENTION: USING THE SAME
CURRENT PILLING DATE: 2002-09-25
CURRENT FILLING DATE: 2001-02-14
PRIOR PAPLICATION NUMBER: 60/265,306
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR PELLING DATE: 2001-01-18
PRIOR PILLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-16
PRIOR PELLING DATE: 2001-10-18
PRIOR PELLING DATE: 2001-10-18
PRIOR PELLING DATE: 2001-01-16
PRIOR PELLING DATE: 2001-10-18
PRIOR PELLING DATE: 2001-10-18
PRIOR PELLING DATE: 2001-10-18
PRIOR PELLING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 269
NUMBER OF SEQ ID NOS: 269
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAP1) GENE DISRUPTIONS
FILE REPERENCE: R-490
CURRENT PILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/280,509
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-08-08
SOFTWARE: FRASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 39; DB 15; Length 285; 75.0%; Pred. No. 75;
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Publication No. US20030167484A1
GENERAL INFORMATION:
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Best Local Similarity 75.v.
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Best Local Similarity 75.0
Matches 6; Conservative
Ellerman, Karen
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; ORGANISM: Mus musculus
US-10-051-874-89
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43 PRITGGGS 50
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Sequence 8, Application US/10405231;
Publication No. US20030190328A1;
GENERAL INFORMATION:
APPLICANT: Diamond, Don J.
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS;
FILE REFERENCE: 1954-346;
CURRENT APPLICATION NUMBER: US/10/405,231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HCWV- REACTIVE T CELLS AND USES THEREFOR TITLE OF INVENTION: HCWV- REACTIVE T CELLS AND USES THEREFOR ITLE REPERRNER: 1954-398 CURRENT APPLICATION NUMBER: US/10/238,607 CURRENT APPLICATION NUMBER: US 09/692,170 PRIOR PEDITORION NUMBER: US 09/692,170 PRIOR PEDITORION NUMBER: US 09/534,639 PRIOR FILING DATE: 2000-10-20 PRIOR PEDITORION NUMBER: US 09/075,257 PRIOR PEDITORION NUMBER: US 09/075,257 PRIOR PILING DATE: 1998-05-11 PRIOR PILING DATE: 1998-05-11 PRIOR APPLICATION NUMBER: US 09/021,298 PRIOR PILING DATE: 1998-11-11 PRIOR APPLICATION NUMBER: US 08/950,064 PRIOR PILING DATE: 1997-10-14 PRIOR PILING DATE: 1997-10-14 PRIOR PILING DATE: 1996-11-12 NUMBER OF SEC 1D NOS: 43
                                                                                                                                                                                                            Query Match 100.0%; Score 53; DB 14; Length 579; Best Local Similarity 100.0%; Pred. No. 0.68; Matches 10; Conservative 0; Mismatches 0. 7-2-3
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                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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; OTHER INFORMATION: Xaa = L, F or M US-10-238-607-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10238607
Publication No. US20030118602A1
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
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Best Local Similarity luv...
And 9; Conservative
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Berencsi, Klara
Kari, Csaba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
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ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
RILING DATE: 19-Aug-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: US/09/171,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10223538
Publication No. US20030120060A1
GENERAL INFORMATION:
The Wistar Institute of, Anatomy & Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                             FILING DATE: 19-Jan-199
FILING DATE: 19-Jan-199
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: KOGTOÉÉ, Cathy A.
REGISTATION NUMBER: WST66APCT
TELECOMMUNICATION INFORMATION:
TELEFAK: 215-540-9200
TELEFAK: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-223-538-6
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STATE: Pennsylvania
COUNTRY: USA
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Matches 10; Conserv
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Paguence 7, Application US/10405231
Publication No. US20030190328A1
GENERAL INFORMATION:
APPLICANT: Diamond, Don J.
IIILE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
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Patent No. US20020058038A1

GRENEAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
FILE REPERRECE: GZ 209500
CURRENT APPLICATION NUMBER: US/09/812,079A

CURRENT APPLICATION NUMBER: 60/191,050

PRIOR FILING DATE: 2000-03-21
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CURRENT APPLICATION NUMBER: US/10/405,231
CURRENT FILING DATE: 2003-04-03
PRIOR FILING DATE: 2003-04-03
PRIOR PILING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
PRIOR PILING DATE: 1998-02-10
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1996-02-10
PRIOR PILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PARENTIN VERSION 3.1
LENGTH: 10
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PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
                                                                                                                           TYPE: PRT ORGANISM: Human cytomegalovirus
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PRIOR FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
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nes 10; Conserv
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                                                                                                    LENGTH: 10
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Matches
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Xari, Csaba Xari, Csaba TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and Uses Therefor
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UGENOTE 2, Application US/10434982

Sequence 2, Application US/10434982

PUBLICATION NO. US20030199673A1

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles A.

TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS COMPOUNDS

TILE REFERENCE: 5018C

CURRENT APPLICATION NUMBER: US/10/434,982

CURRENT FILING DATE: 2003-05-10

PRIOR APPLICATION NUMBER: US 60/191,050

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 2

LENGTH: 561
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                                                                                                                                                 100.0%; Score 53; DB 9; Length 561; 100.0%; Pred. No. 0.66; tive 0; Mismatches 0; Indels
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APPLICANT: The Wistar Institute of, Anatomy & Biology
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
SOFTWARE: FaetSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 561
TYPE: PRT
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ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10223538 Publication No. US20030120060A1
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Berencsi, Klara
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STATE: Pennsylvania
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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US-10-434-982-2
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                                                                                       ORGANISM: Homo sapiens
                                                                                                             US-09-812-079A-2
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	Sequence 432, App Sequence 432
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GenCore version 5.1.6
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BLOSUM62 Sequence:

Scoring table:

Gapop 10.0 , Gapext 0.5

809742 seqs, 211153259 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 500 summaries

Published_Applications_AA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli	Seguence 2, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 8, Appli	æ	Sequence 89, Appl	Sequence 2, Appli	Sequence 86, Appl	Sequence 87, Appl	Sequence 124, App	Sequence 2854, Ap	Sequence 109, App
	ID	US-10-238-607-7	US-10-405-231-7	US-09-812-079A-2	US-10-434-982-2	US-10-223-538-6	US-10-223-538-8	US-10-238-607-8	US-10-405-231-8	US-10-051-874-89	US-10-109-616-2	US-10-051-874-86	US-10-051-874-87	US-10-259-194A-124	15 US-10-374-780A-2854	US-10-306-762-109
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Sequence 12713, A Sequence 13012, A Sequence 13012, A Sequence 15056, A Sequence 15056, A Sequence 15024, A Sequence 20021, A Sequence 20021, A Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 14, Appli Sequence 17, Appli Sequence 21, Appli Sequence 13, Appli Sequence 197, Appli Sequence	ance III
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